

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 17:57:31 ; Search time 5526 Seconds
(without alignments)
10859.687 Million cell updates/sec

Title: US-10-018-030B-1

Perfect score: 1269
Sequence: 1 atggctgcagctagctgac.....tggacctgacaggtctctaa 1269

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 segs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_atg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_dr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1269	100.0	1269	6	BD276253
2	1095.4	86.3	2244	9	BD276253 VARIANTS
3	1020.4	80.4	2298	9	BS538160 Homo sapi
4	1020.4	80.4	2307	9	BC043492 Homo sapi
5	1020.4	80.4	2330	9	BC032410 Homo sapi
6	1020.4	80.4	2330	9	BC033810 Homo sapi
7	1008	79.4	1011	6	BC064662 Homo sapi
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9	959.6	75.6	2262	6	BD276254 VARIANTS
10	959.6	75.6	2262	6	BD276255 VARIANTS
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14	855.6	67.4	2094	9	AX335498 Sequence
15	855.6	67.4	2094	9	HSU25297
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18	701	55.2	2121	6	BC003801 Mus muscu
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					AR034585 Sequence
					166263 Sequence 3

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24	670	52.8	1561	10	AP027570	AP027570 Mus muscu
25	647	51.0	1450	10	BC060625	BC060625 Mus muscu
26	582.2	45.9	979	6	AX677670	AX677670 Sequence
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45	226.6	17.9	1758	5	BC070713	BC070713 Xenopus 1

ALIGNMENTS

RESULT 1
LOCUS BD276253 1269 bp DNA linear PAT 17-JUL-2003
DEFINITION VARIANTS OF TRAP2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING
PATHWAY.
ACCESSION BD276253
VERSION BD276253.1 GI:33086021
KEYWORDS JP 2002542826-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1269)
Ivashchenko,Y.D., Ill.G.H.S., Pagnoni,M.F., Guo,K. and Clark,K.L.
VARIANTS OF TRAP2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING
PATHWAY
JOURNAL Patent: JP 2002542826-A 1 17-DEC-2002;
Avantis Pharmaceuticals Products Inc,George H Seafoss III, Marco F
Pagnoni,Yuri D Ivashchenko,Kun Guo,Kenneth L Clark
COMMENT OS Homo sapiens
PN JP 2002542826-A/1
PD 17-DEC-2002 JP 2000615761
PF 06-APR-2000 JP 2000615761
PI 30-APR-1999 US 60/131940
PI Yuri d Ivashchenko,George h seafoss III,marco f pagnoni,kun
guo,
PI Kenneth l clark
CC
FH
FEATURES
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 ACCESSION
 VERSION
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 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2244)
 Ottenwelder, B., Obermaier, B., Deutschenbur, S., Mewes, H.W., Well, B., Amid, C., Oesinger, A., Fodor, G., Han, M., and Wiemann, S.
 Direct Submision
 Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 Sequenced by Medigenomix (Martinried/germany) within the CDNA Sequencing Consortium of the German Genome Project. This clone (DKFZp686H1465) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de. Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cdna/>.
 FEATURES
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Best Local Similarity 88.6%; Pred. No. 9.5e-218;
Matches 1268; Conservative 0; Mismatches 1; Indels 162; Gaps 1;

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RESULT 3
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DEFINITION Homo sapiens TNF receptor-associated factor 2, mRNA (cDNA clone MGC:49872 IMAGE:5767794), complete cds.
ACCESSION BC043492
VERSION BC043492.1 GI:28175371
KEYWORDS MGC.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2298)
Strasberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schneider, C.F., Bhac, N.K., Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Cantoni, P., Prange, C., Raha, S., Locus, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, J.J., Huyl, S.W., Villalón, D.K., Mazny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalka, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2298)
Strasberg, R.
Direct Submission
Submitted (09-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.

REMARK
COMMENT

USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@gscc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Buterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan North,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabhu,
Parvaneh Saeedi, Jr Santos, Angeliq Schnerch, Ursula Skalska,
Diane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

FEATURES
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ORIGIN

Query Match 80.4%; Score 1020.4; DB 9; Length 2298;
Best Local Similarity 84.2%; Pred. No. 4e-202;
Matches 1268; Conservative 0; Mismatches 1; Indels 237; Gaps 1;
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RESULT 4
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 ACCESSION BC032410
 VERSION BC032410.1 GI:21619569
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2307)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477922
 2 (bases 1 to 2307)
 Strausberg, R.
 Direct Submission
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>

TITLE
 JOURNAL
 PUBMED
 REVERSE
 AUTHORS
 JOURNAL

REWARD
 COMMENT

Query Match 80.4%; Score 1020.4; DB 9; Length 2307;
 Best Local Similarity 84.2%; Pred. No. 4e-202;
 Matches 1268; Conservative 0; Mismatches 1; Indels 237; Gaps 1;
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ORIGIN
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 Best Local Similarity 84.2%; Pred. No. 4e-202;
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CONTACT: nisc.mgc@nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
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 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 64 Row: 1 Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 22027613.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 68 Row: 1 Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22027611.

FEATURES

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Location/Qualifiers
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/clone.lib="NIH_MGC_116"
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/note="vector: pCMV-SPORT6"

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Query Match	80.4%;	Score 1020.4;	DB 9;	Length 2320;
Best Local Similarity	84.2%;	Pred. No. 4e-202;		
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Db	406	TACGAGAGCTGCCACGAGGCGCTGCCCGCTCATGCTGACCGAATGTCCCGCTGCAAA	465	
QY	365	-----	364	

Db	466	GGCCTGGTCCGCTTGGTGTGAAAAAGGAGCGCCACCTGGAGCACGAGTCCCGGAGAGAAGC	525
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Db	526	CTGAGCTGCCGGCATTGCCGGCACCCCTGCTCGGAGCAGACGTGAGGCGCACCCAG	585
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Qy	365	-AGTTTCAGGACCACGTCACAGACTTGTGGCAAGTGTGAGTCCCTTGACAGATCCACGCC	423
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Qy	424	ATCGCTGCTCTGAGACGGTAGAGGTGAGAAACAGCAGGAGCAGGAGTGCGAGTGGCTG	483
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Qy	544	CAGAGCCACCGGGGTCCAGAGTCTCTGCAAGGTGCGAGAGCTTGAGAAAGACCGGCC	603
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Homo sapiens (human)			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 1011)			

AUTHORS		Ivashchenko,Y.D., Iii,G.H.S., Pagnoni,M.F., Guo,X. and Clark,K.L.	
TITLE		VARIANTS OF TRAF2 WHICH ACT AS AN INHIBITOR OF TNF-ALPHA SIGNALING	
JOURNAL		PATHWAY	
COMMENT		Patent: JP 2002542826-A 2 17-DEC-2002;	
		Avantis Pharmaceuticals Products Inc,George H Searfoss III, Marco F	
		Pagnoni,Yuri D Ivashchenko,Kun Guo,Kenneth L Clark	
		OS Homo sapiens	
		PN JP 2002542826-A/2	
		PD 17-DEC-2002	
		PF 06-APR-2000 JP 2000615761	
		PR 30-APR-1999 US 60/131940	
		PI yuri d ivashchenko,george h searfoss iii,marco f pagnoni,kun	
		PI Guo,	
		PI Kenneth l clark	
		CC	
FEATURES		Location/Qualifiers.	
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		Best Local Similarity 100.0%; Pred. No. 1 6e-199;	
		Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	262	AGTTTCGGCTTCCAGATAATGTGCCCCGAGGAGGTGAGAGCCTGCGGCGCTGTGT	321
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Qy	322	CCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	381
Db	64	CCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	123
Qy	382	AAGACTTGTGGCAAGTTCGAGTCCCTTGAGATTTCACGCCATCGGCTCGCTGAGACG	441
Db	124	AAGACTTGTGGCAAGTTCGAGTCCCTTGAGATTTCACGCCATCGGCTCGCTGAGACG	183
Qy	442	GTAGAGGTTGAGAAACAGCAGGAGCAGAGTGCAGTGGCTGCGGGAGCAGCTGGCCATG	501
Db	184	GTAGAGGTTGAGAAACAGCAGGAGCAGAGTGCAGTGGCTGCGGGAGCAGCTGGCCATG	243
Qy	502	CTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTGGAGACCAAGCCAGCCAGCGGGGTCA	561
Db	244	CTACTGAGCTCGGTGCTGGAGGCAAGCCCTCTTGGAGACCAAGCCAGCGGGGTCA	303
Qy	562	GAGTCTCTGAGAGGTGCGAGAGCTTGGAGAAAGACGGCCACTTTTGAGAAACATTGTC	621
Db	304	GAGTCTCTGAGAGGTGCGAGAGCTTGGAGAAAGACGGCCACTTTTGAGAAACATTGTC	363
Qy	622	TGCTCTCTGAACCGGGAGGTGGAGAGGTGCGCATGACTCCGAGGCTCGAGCCGCGAG	681
Db	364	TGCTCTCTGAACCGGGAGGTGGAGAGGTGCGCATGACTCCGAGGCTCGAGCCGCGAG	423
Qy	682	CACCGGCTGGAACCAAGACAAAGATTGAAGCCCTGAGTAGCAAGGTGCAAGCTGGAGAGG	741
Db	424	CACCGGCTGGAACCAAGACAAAGATTGAAGCCCTGAGTAGCAAGGTGCAAGCTGGAGAGG	483
Qy	742	AGCATTCGCTCAAGGACCTGGCGATGCTGACTTGGAGCAGAGGTCTTGGAGATGGAG	801
Db	484	AGCATTCGCTCAAGGACCTGGCGATGCTGACTTGGAGCAGAGGTCTTGGAGATGGAG	543
Qy	802	GCATCCACCTACGATGGGTCTTCACTCTGGAAGATCTCAGACTTTCGCCAGAAAGCTCCAG	861
Db	544	GCATCCACCTACGATGGGTCTTCACTCTGGAAGATCTCAGACTTTCGCCAGAAAGCTCCAG	603
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Db 1555 CTCTAA 1560

RESULT 10
AR211089
LOCUS AR211089 2262 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 2 from patent US 6399297.
ACCESSION AR211089
KEYWORDS AR211089.1 GI:21514318
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2262)
AUTHORS Baker,B.F., Cowser,L.M., Monia,B.P. and Xu,X.S.
TITLE Antisense modulation of expression of tumor necrosis factor receptor-associated factors (TRAFs)
JOURNAL Patent: US 6399297-A 2 04-JUN-2002;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 75.6%; Score 959.6; DB 6; Length 2262;
Best Local Similarity 81.7%; Pred.No.1.8e-189;
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Qy 361 TACG----- 364

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Qy 1264 CTCTAA 1269

Db 1555 CTCTAA 1560

RESULT 11

AX333704

LOCUS AX333704 2262 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 4213 from Patent WO0194629.

ACCESSION AX333704

VERSION AX333704.1 GI:18124423

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Cancer gene determination and therapeutic screening using signature gene sets

JOURNAL Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.

FEATURES

Avallon Pharmaceuticals (US)

Location/Qualifiers

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/organism="Homo sapiens"

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ORIGIN

Query Match 75.6%; Score 959.6; DB 6; Length 2262;

Best Local Similarity 81.7%; Pred. No. 1.8e-189;

Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

Qy 1 ATGGCTGCAGCTAGCTAGTACCCCTCCCTGGCTCCTGGAGTGTGACGCCGGCTCTCC 60

Db 55 ATGGCTGCAGCTAGCTAGTACCCCTCCCTGGCTCCTGGAGTGTGACGCCGGCTCTCC 114

Qy 61 AAGACCTCTCTGGGGACCAAGCTGGAAGCAAGTACTGTCTCCCTGACAGAAACGTC 120

Db 115 AAGACCTCTCTGGGGACCAAGCTGGAAGCAAGTACTGTCTCCCTGACAGAAACGTC 174

Qy 121 CTCGCGAGGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGTCTCTCTGCTGGCCAGC 180

Db 175 CTCGCGAGGCCCTTCCAGGCGCAGTGTGGCCACCGGTACTGTCTCTCTGCTGGCCAGC 234

Qy 181 ATCTCAGCTCTGGCTCAGAACTGTGCTGCTGCTGTTTACAGAGGCAATATGAGAA 240

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Qy 1264 CTCTAA 1269

Db 1555 CTCTAA 1560

RESULT 12

AX335498

LOCUS AX335498 2262 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 6007 from Patent WO0194629.

ACCESSION AX335498

MEDLINE 95366958
PUBMED 7639698
REFERENCE 2 (bases 655 to 1560)
AUTHORS Rothe,M., Wong,S.C., Henzel,W.J. and Goeddel,D.V.
TITLE A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor
JOURNAL Cell 78 (4), 681-692 (1994)
MEDLINE 94349371
PUBMED 8069916
REFERENCE 3 (bases 1 to 2262)
AUTHORS Song,H.Y.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1994) Ho Y. Song, Physiology and Walther Oncology Center, Indiana University School of Medicine, 975 W. Walnut St., Indianapolis, IN 46202, USA
COMMENT On Sep 6, 1995 this sequence version replaced gi:695148.
FEATURES
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Best Local Similarity 81.7%; Pred. No. 1.8e-189;
Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;
QY 1 ATGGCTGCAGTAGCTGACCCCTCCCTGGCTCCCTGGAGTTGCTACAGCCCGCTTCCTCC 60
Db 55 ATGGCTGCAGTAGCTGACCCCTCCCTGGCTCCCTGGAGTTGCTACAGCCCGCTTCCTCC 114
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Qy 1264 CTCTAA 1269
Db 1555 CTCTAA 1560

RESULT 14
AX113379
LOCUS AX113379 2094 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 63 from Patent EP1293569.
ACCESSION AX113379
VERSION AX113379.1 GI:29888235
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yanamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tanechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and
Masuho, Y.

TITLE Full-length cDNAs
JOURNAL Patent: EP 1293569-A 63 19-MAR-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
LOCATION/Qualifiers
source 1. 2094
/organism="Homo sapiens"
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FEATURES
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Best Local Similarity 81.5%; Pred. No. 8.3e-168;
Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6;
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ACCESSION    AK054686
VERSION      AK054686.1 GI:16549280
KEYWORDS     Oligo capping; fis (full insert sequence).
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
  AUTHORS   Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
            Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
            Sekine, M., Oabayashi, M., Nishi, T., Shibahara, T., Tanaka, H.,
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            Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
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            Nakai, K., Tada, Y., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
            Complete sequencing and characterization of 21,243 full-length
            human cDNAs
            Nat. Genet. 36 (1), 40-45 (2004)
            14702039
  TITLE     Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
            Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
            Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
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            Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
            Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
            NEDO human cDNA sequencing project
  JOURNAL   Unpublished
  PUBLISHED 3 (bases 1 to 2094)
  REFERENCE 1
  AUTHORS   Isogai, T., Otsuki, T. and Sugiyama, T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@nri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
            NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB
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Query Match      67.4%; Score 855.6; DB 9; Length 2094;
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Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6;

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QY   61 AAGACCCCTCTCTGGGAGCAAGCTGGAAGCAAGTACCTGTCTCCGCTGCAGAAAGCTC 120
DB   105 AAGACCCCTCTCTGGGAGCAAGCTGGAAGCAAGTACCTGTCTCCGCTGCAGAAAGCTC 164
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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ALIGNMENTS

RESULT 1

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ID AAD01947 standard; cDNA; 2025 BP.

XX AAD01947;

DT 26-MAR-2001 (first entry)

XX Human TRAF2 splice variant TRAF2TR (TRAF2 truncated) cDNA.

XX Human: tumour necrosis factor; TNF; TRAF2-FL; inhibitor; treatment;
TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
anti-inflammatory; cardiac; myocardial infarction; splice variant;
vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
rheumatoid arthritis; immunosuppressive; Crohn's disease; psoriasis;
non-insulin dependent diabetes; inflammatory bowel disease; stroke;
neurodegenerative disease; ss.

XX Homo sapiens.

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XX Key Location/Qualifiers

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XX /note= "This region is specifically claimed in claim 1"

XX WO200006737-A1.

XX 09-NOV-2000.

XX 06-APR-2000; 2000WO-US009178.

XX 30-APR-1999; 99US-0131940P.

XX (AVET) AVENTIS PHARM PROD INC.

XX Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;

XX WPI; 2001-007223/01.

XX P-PSDB; AAY1901.

XX New nucleic acid encoding variants of tumor necrosis factor receptor
associated factors useful for inhibiting tumor necrosis factor alpha-

PT regulated pathways, and for treating Crohn's disease, psoriasis, and
 PF rheumatoid arthritis.
 XX Claim 1; Fig 4a; 74pp; English.
 XX The present sequence is a cDNA encoding tumour necrosis factor (TNF)-
 CC receptor associated factor-truncated protein (TRAF2TR) which is a splice
 CC variant of human TRAF2 protein. TRAF2TR has an ability to inhibit TNF
 CC alpha signalling pathways. The TRAF2TR variant is useful for inhibiting
 CC diseases involving overproduction of TNFalpha, TNFalpha pathologies
 CC involving hyperactivation of nuclear factor kappa B (NFkB). The variant
 CC is also useful for inhibiting and treating inflammatory processes
 CC involving TNFalpha such as Crohn's disease, psoriasis, rheumatoid
 CC arthritis, graft versus host disease, Crohn's disease, Crohn's disease,
 CC inflammatory bowel disease, and neurodegenerative diseases or
 CC cardiovascular disease such as cardiac ischaemia-reperfusion injury
 CC following myocardial infarction, coronary artery bypass surgery, cardiac
 CC transplantation or ischaemia-reperfusion injury in the central nervous
 CC system (CNS) following stroke, the progression and rupture of advanced
 CC coronary atherosclerotic plaques, development and progression of
 CC congestive heart failure, endothelial cell injury following balloon
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 XX
 DT 26-MAR-2001 (first entry)
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 DE Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
 KW TNF-receptor associated factor; TRAF2 truncated-deleted; TRAF2TD;
 KW antiinflammatory; cardiant; mutant; muten; myocardial infarction;
 KW vasotropic; antipsoriatic; antirheumatic; antidiabetic;
 KW antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 KW rheumatoid arthritis; immunosuppressive; Crohn's disease; psoriasis;
 KW non-insulin dependent diabetes; graft versus host disease; cardiovascular disease;
 KW neurodegenerative disease; variant; TRAF2 truncated; TRAF2TR; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
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 FT CDS /tag= a
 FT /product= "TRAF2TD protein"
 XX
 PN W0200066737-A1.

XX 09-NOV-2000.
 XX 06-APR-2000; 2000WO-US0009178.
 XX 30-APR-1999; 99US-0131940P.
 XX (AVET) AVENTIS PHARM PROD INC.
 XX Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
 XX WPI; 2001-007223/01.
 XX P-PSDB; AAY71902.
 XX New nucleic acid encoding variants of tumor necrosis factor receptor
 XX associated factors useful for inhibiting tumor necrosis factor alpha-
 XX regulated pathways, and for treating Crohn's disease, psoriasis, and
 XX rheumatoid arthritis.
 XX Claim 2; Fig 3a; 74pp; English.
 XX The present sequence is a cDNA encoding tumour necrosis factor (TNF)-
 XX receptor associated factor truncated-deleted (TRAF2TD) protein which is a
 XX variant of human TRAF2TR (truncated). This sequence includes both the
 XX naturally occurring splice variation and a deletion at the 5' end of
 XX human TRAF2-FL (full-length) nucleic acid sequence. TRAF2TD has an
 XX ability to inhibit TNF alpha signalling pathways. The TRAF2TD variant is
 XX useful for inhibiting diseases involving over production of TNFalpha, B
 XX TNFalpha pathologies involving hyperactivation of nuclear factor kappa B
 XX (NFkB). The variant is also useful for inhibiting and treating
 XX inflammatory processes involving TNFalpha such as Crohn's disease,
 XX psoriasis, rheumatoid arthritis, graft versus host disease, non-insulin
 XX dependent diabetes, inflammatory bowel disease, and neurodegenerative
 XX diseases or cardiovascular disease such as cardiac ischaemia-reperfusion
 XX injury following myocardial infarction, coronary artery bypass surgery,
 XX cardiac transplantation or ischaemia-reperfusion injury in the central
 XX nervous system (CNS) following stroke, the progression and rupture of
 XX advanced coronary atherosclerotic plaques, development and progression of
 XX congestive heart failure, endothelial cell injury following balloon
 XX angioplasty, or apoptotic cell death of myocardial cells
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Query Match 79.4%; Score 1008; DB 5; Length 1011;
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QY 382 AGACTTTGGCAAGTGTGAGTCCCTTCAGATTCCAGCCCATGGCTGCTCGAGACG 441
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QY 442 GTAGAGGGTGAAGAAACAGCAGGAGCAGCAGGTGTCAGTGGCTCGGGAGCACTCGGCCATG 501
 DB 184 GTAGAGGGTGAAGAAACAGCAGGAGCAGCAGGTGTCAGTGGCTCGGGAGCACTCGGCCATG 243

QY 502 CTACTGAGTCCGGTGTGAGGCAAGCCCTCTTTGGGAGACACAGGACCGCGGGTCA 561
 DB 244 CTACTGAGTCCGGTGTGAGGCAAGCCCTCTTTGGGAGACACAGGACCGCGGGTCA 303

QY 562 GAGCTCTCCAGAGGTGCGAGAGCTGGAGAGAGAGAGCGCCACTTTTGAACAATTGTC 621
 DB 304 GAGCTCTCCAGAGGTGCGAGAGCTGGAGAGAGAGAGCGCCACTTTTGAACAATTGTC 363

QY 622 TCCGTCCTGAAACCGGAGGTGGAGGGTGGCCATCACTGCCAGGCTCGAGCGCGGAG 681

DB 364 TGGTCTCTGAACCCGGAGGTGGAGAGGGTGCCCATGACTGCCAGGCGCTGCAGCCGCGAG 423
 QY 682 CACCGGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAAGGTGCGACAGCTGGAGAGG 741
 DB 424 CACCGGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAAGGTGCGACAGCTGGAGAGG 483
 QY 742 AGCATTGGCCCTCAAGGACCTGGCGATGGCTGACCTTGGAGCAAGAGGCTTTGGAGATGGAG 801
 DB 484 AGCATTGGCCCTCAAGGACCTGGCGATGGCTGACCTTGGAGCAAGAGGCTTTGGAGATGGAG 543
 QY 802 GCATCCACCTACGATGGGGTCTTTCATCTGGAAGATCTCAGACTTCCGCCAGGAAGCTCCAG 861
 DB 544 GCATCCACCTACGATGGGGTCTTTCATCTGGAAGATCTCAGACTTCCGCCAGGAAGCTCCAG 603
 QY 862 GAAGCTGTGGTGGCGCGCATACCGCCCATCTTCTCCCGAGCCTTCTACACAGCAGGTAC 921
 DB 604 GAAGCTGTGGTGGCGCGCATACCGCCCATCTTCTCCCGAGCCTTCTACACAGCAGGTAC 663
 QY 922 GGCTACAAGATGTCTGCGGTATCTACCTGAACGGCGACGGCACCGGGCGAGGAACACAC 981
 DB 664 GGCTACAAGATGTCTGCGGTATCTACCTGAACGGCGACGGCACCGGGCGAGGAACACAC 723
 QY 982 CTGTCCCTCTTCTTTGTGGTGAAGAGGGCCCGAATGACCCCTGTGCGGTGGCCCTTC 1041
 DB 724 CTGTCCCTCTTCTTTGTGGTGAAGAGGGCCCGAATGACCCCTGTGCGGTGGCCCTTC 783
 QY 1042 AACAGAGAGGTGACCTTAATGCTGCTCGACCAAGATAACCGGGAGCACTGATTGAGCC 1101
 DB 784 AACAGAGAGGTGACCTTAATGCTGCTCGACCAAGATAACCGGGAGCACTGATTGAGCC 843
 QY 1102 TTCAGGCGCCAGCTGACTTTCATCTCTTTTCAGAGGCGAGTCAACGACATGAACATCGCA 1161
 DB 844 TTCAGGCGCCAGCTGACTTTCATCTCTTTTCAGAGGCGAGTCAACGACATGAACATCGCA 903
 QY 1162 AGCGCTGCGCCCTCTTCTGCGCCCGTCTCCAAGATGAGGCAAGAAATTCCTACGTGCGG 1221
 DB 904 AGCGCTGCGCCCTCTTCTGCGCCCGTCTCCAAGATGAGGCAAGAAATTCCTACGTGCGG 963
 QY 1222 GACCATGCCATCTTTCATCAAGGGCATTGTGACCTGACAGGGCTCTAA 1269
 DB 964 GACCATGCCATCTTTCATCAAGGGCATTGTGACCTGACAGGGCTCTAA 1011

RESULT 3
 ACF04633
 ID ACF04633 standard; DNA; 1506 BP.
 AC ACF04633;
 XX 18-DEC-2003 (first entry)
 DE TRAF2 protein coding sequence.
 KW TRAF2; inflammatory response; rheumatoid arthritis; LtbetaP;
 KW lymphocytin-beta receptor; modulator; cancer; immunological disease;
 KW apoptosis; cytostatic; immunosuppressive; antirheumatic; antiarthritic;
 KW antiinflammatory; dermatological; nephrotropic; antithyroid;
 KW thyromimetic; muscular-Gen; neuroprotective; antianaemic; haemostatic;
 KW vasotropic; antidiabetic; gene; ds.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 CDS 1..1506
 FT /*tag= a
 FT /product= "TRAF2"
 XX
 PN WO2003066834-A2.
 XX
 XX 14-AUG-2003.
 XX
 XX 10-FEB-2003; 2003WO-US003923.
 XX
 XX

OR-FEB-2002; 2002US-0355183P.
 (AMHP) WYETH.
 Kuai J, Wooters JL, Nickbarg BB, Qiu Y, Lin L;
 WPI; 2003-748125/70.
 P-PSDB; ABR84599.
 New purified lymphotoxin-beta receptor protein complex, useful for
 identifying modulators of lymphotoxin-beta receptor activity or
 expression for treating or preventing cancer or an autoimmune disorder,
 e.g. vasculitis or diabetes.
 Disclosure; Page 6; Opp; English.
 The present invention relates to a purified complex comprising a
 lymphotoxin beta receptor (LbtaR) polypeptide and Smac polypeptide. The
 lymphotoxin-beta receptor (LbtaR) complex is useful for identifying
 modulators of LbtaR activity or expression for treating or preventing
 cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid
 arthritis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's
 disease, Hashimoto's thyroiditis, pemphigus vulgaris, myasthenia gravis,
 scleroderma, autoimmune haemolytic anaemia, autoimmune thrombocytopenic
 purpura, polymyositis, dermatomyositis, pernicious anaemia, Sjogren's
 syndrome, ankylosing spondylitis, vasculitis, or type I diabetes
 mellitus. The present sequence is the coding sequence of a TRAF2 protein,
 which forms part of the complex of the invention
 Sequence 1506 BP; 317 A; 453 C; 460 G; 276 T; 0 U; 0 Other;
 Query Match 75.6%; Score 959.6; DB 10; Length 1506;
 Best Local Similarity 81.7%; Pred. No. 1.7e-205;
 Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;
 QY 1 ATGCTCGAGTACGTGACCCCGCTGGTCCCTGGAGTTGTACAGCCCGCTTCTCC 60
 DB 1 ATGCTCGAGTACGTGACCCCGCTGGTCCCTGGAGTTGTACAGCCCGCTTCTCC 60
 QY 61 AAGACCTCTCTGGGGACCAAGCTGGAACCAAGTACCTGTCTCCGCTCGAAGACGTC 120
 DB 61 AAGACCTCTCTGGGGACCAAGCTGGAACCAAGTACCTGTCTCCGCTCGAAGACGTC 120
 QY 121 CTCGAGGCGCTTCAGGCGCAGTGGCCACCGTACTGCTCTCTCTGCTGGCCAGC 180
 DB 121 CTCGAGGCGCTTCAGGCGCAGTGGCCACCGTACTGCTCTCTCTGCTGGCCAGC 180
 QY 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGCTTTCAGGAGGTCATATGAAGAA 240
 DB 181 ATCTCTAGCTCTGGGCTCAGAACTGTGCTGCTGCTTTCAGGAGGTCATATGAAGAA 240
 QY 241 GGCAATTTCTATTAGAAAGCAGTTCGGCTTCCAGATATGCTGCTCCCGCAGGAGGTG 300
 DB 241 GGCAATTTCTATTAGAAAGCAGTTCGGCTTCCAGATATGCTGCTCCCGCAGGAGGTG 300
 QY 301 GAGAGCTGCGGCGCTGTGTCAGTGTGATGACCTGGAAGGGGACCTCGAAAGAA 360
 DB 301 GAGAGCTGCGGCGCTGTGTCAGTGTGATGACCTGGAAGGGGACCTCGAAAGAA 360
 QY 361 TACG----- 364
 DB 361 TACGAGAGCTGCCACGAAGGCGGTGCTGCTCATGCTGACCGAATGCTCCCGGTGTAA 420
 QY 365 ----- 364
 DB 421 GGCTGCTGCGCTTGTGTAAGAGGCGGCACTGGAGCAGAGTCCCGGAGAGAGC 480
 QY 365 ----- 364
 DB 481 CTGAGCTGCGGCGATTGCGGGGACCTGTGTCGAGAGCAGTGAAGGCGCACCAGAG 540
 QY 365 ----- 364

DB 541 GTCTGCCCAAGTTCCCTTAACCTTGTGACGGCTGCGGCAAGAGAGATCCCGCGGAG 600
 QY 365 -AGTTTCAGGACCAAGTTCAGAGCTTGTGGCAAGTGTGAGTCCCTTTCAGATTCACGCC 423
 DB 601 AAGTTTCAGGACCAAGTTCAGAGCTTGTGGCAAGTGTGAGTCCCTTTCAGATTCACGCC 660
 QY 424 ATCGCTGCTCTGAGACGGTGTAGAGGGTGTAGAAACAGCAGGAGACGAGGTGCTGCTG 483
 DB 661 ATCGCTGCTCTGAGACGGTGTAGAGGGTGTAGAAACAGCAGGAGACGAGGTGCTGCTG 720
 QY 484 CGGAGACCTTGGCCATCTACTAGCTCGGTGTGAGGCAAGGCGCCCTTCTTGGAGAC 543
 DB 721 CGGAGACCTTGGCCATCTACTAGCTCGGTGTGAGGCAAGGCGCCCTTCTTGGAGAC 780
 QY 544 CAGAGCCACGCGGGGTGTAGAGCTCTCTGAGAGGTGCGAGAGCTTGGAGAAAGACGCGC 603
 DB 781 CAGAGCCACGCGGGGTGTAGAGCTCTCTGAGAGGTGCGAGAGCTTGGAGAAAGACGCGC 840
 QY 604 ACTTTTGAGAACATTTCTGCTGCTCTGAAACCGGAGGTGTGAGAGGTGCGCCATCACTGCC 663
 DB 841 ACTTTTGAGAACATTTCTGCTGCTCTGAAACCGGAGGTGTGAGAGGTGCGCCATCACTGCC 900
 QY 664 GAGGCTCTGAGCCGCGCAGCACCCTGTGACCAAGATTTGAAGCCCTGTAGTAGCAAG 723
 DB 901 GAGGCTCTGAGCCGCGCAGCACCCTGTGACCAAGATTTGAAGCCCTGTAGTAGCAAG 960
 QY 724 GTGAGCAGCTGTGAGAGAGCATTTGGCTCTAAGGACCTTGGGATGTGCTGAGTGGAGCAG 783
 DB 961 GTGAGCAGCTGTGAGAGAGCATTTGGCTCTAAGGACCTTGGGATGTGCTGAGTGGAGCAG 1020
 QY 784 AAGGCTTTGGAGATGGAGGATCCACCTACGATGGGTCTTTCATCTGGAAGATCTCAGAC 843
 DB 1021 AAGGCTTTGGAGATGGAGGATCCACCTACGATGGGTCTTTCATCTGGAAGATCTCAGAC 1080
 QY 844 TTGCGCAGGAAAGTCCAGGAAGCTGTGCTGGCGCATACCCGCCATCTTCTCCCGAGCC 903
 DB 1081 ATCTCTCAGGAAGTCCAGGAAGCTGTGCTGGCGCATACCCGCCATCTTCTCCCGAGCC 1140
 QY 904 TTCTACACAGCAGGTAGGCTCAAGATGTGTCTGGTATCTACCTGAACGGCGAGCGC 963
 DB 1141 TTCTACACAGCAGGTAGGCTCAAGATGTGTCTGGTATCTACCTGAACGGCGAGCGC 1200
 QY 964 ACCGCGCAGGAACACACCTCTCTCTTTTGTGTGTATGAAGGCGCCGAATGACGCC 1023
 DB 1201 ACCGCGCAGGAACACACCTCTCTCTTTTGTGTGTATGAAGGCGCCGAATGACGCC 1260
 QY 1024 CTGCTGCGGTGGCGCTTCAACAGAGAGTGAACCTTATGCTGCTCGACAGAAATACCGG 1083
 DB 1261 CTGCTGCGGTGGCGCTTCAACAGAGAGTGAACCTTATGCTGCTCGACAGAAATACCGG 1320
 QY 1084 GAGCAGCTGATTGAGCGCTTTCAGGCGCCGAGCTGACTTCTCTCTTTTCAGAGGCGCAGTC 1143
 DB 1321 GAGCAGCTGATTGAGCGCTTTCAGGCGCCGAGCTGACTTCTCTCTTTTCAGAGGCGCAGTC 1380
 QY 1144 AACGACATGAACATCGAAGCGGTGCGCCCTCTTCTGCGCGCTCTCCAAAGATGAGGCA 1203
 DB 1381 AACGACATGAACATCGAAGCGGTGCGCCCTCTTCTGCGCGCTCTCCAAAGATGAGGCA 1440
 QY 1204 AAGATTTCTAGTGGCGGAGCATGCCATCTTTCATCAGGCGCATTTGGAGCTGACAGGG 1263
 DB 1441 AAGATTTCTAGTGGCGGAGCATGCCATCTTTCATCAGGCGCATTTGGAGCTGACAGGG 1500
 QY 1264 CTCTAA 1269
 DB 1501 CTCTAA 1506

RESULT 4
 ADM45823
 ID ADM45823 standard; cDNA; 1506 BP.
 XX
 AC
 AC
 XX ADM45823;

QY 1144 AACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCCTCTCCAGATGGAGGCA 1203
 Db 1381 AACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCCTCTCCAGATGGAGGCA 1440
 QY 1204 AAGAAATTCCTACGTGCGGGACGATGCCATCTTCAATCAAGGCCATTGGACCTGACAGGG 1263
 Db 1441 AAGAAATTCCTACGTGCGGGACGATGCCATCTTCAATCAAGGCCATTGGACCTGACAGGG 1500
 QY 1264 CTCTAA 1269
 Db 1501 CTCTAA 1506

RESULT 5
 ID AAA55491 standard; DNA; 2262 BP.
 AC AAA55491;
 XX 30-AUG-2000 (first entry)
 DE Human TRAF2 nucleotide sequence locus name HSU12597.
 XX Tumour necrosis factor receptor-associated factor; TRAF; human;
 KW antisense oligonucleotide; phosphorothioate; antiproliferative;
 KW anti-inflammatory; E-selectin; jun kinase; ds.
 XX Homo sapiens.
 OS
 FN WO20020435-A1.
 PD 13-APR-2000.
 PF 05-OCT-1999; 99WO-US023171.
 PR 06-OCT-1998; 98US-00167109.
 XX (ISIS-) ISIS PHARM INC.
 PI Baker BF, Cowsett LM, Monia BP, Xu XS;
 DR WPI; 2000-303732/26.
 XX P-PSDB; RAY98165.
 PT Antisense oligonucleotides targeted to nucleic acids encoding human tumor
 PT necrosis factor receptor-associated factor (TRAF), useful for treating
 XX diseases associated with TRAF expression such as inflammatory diseases.
 PS Example 16; Page 109-111; 170pp; English.
 XX The present invention relates to antisense oligonucleotides (see AAA55496
 CC -A55757) which are targeted to nucleic acids encoding a human tumor
 CC necrosis factor receptor-associated factor (TRAF). The antisense
 CC sequences comprise at least one modified internucleotide linkage, which
 CC is a phosphorothioate linkage. The oligonucleotides also include at least
 CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
 CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
 CC TRAF1-6. Included in the invention is a method for treating a human
 CC having a disease associated with the expression of TRAF comprising
 CC administering an antisense oligonucleotide. The reduction of jun kinase
 CC activation in cells comprises contacting the cells with an antisense
 CC oligonucleotide targeted to TRAF-6. A method for the reduction of E-
 CC selectin expression in cells or tissues comprises contacting the cells or
 CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
 CC The antisense oligonucleotides have antiproliferative and anti-
 CC inflammatory activity and are useful for treating disorders associated
 CC with cell proliferation and inflammation. The antisense oligonucleotides
 CC may also be used as a diagnostic probe for studying gene function

Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;
 Query Match 75.6%; Score 959.6; DB 3; Length 2262;

Best Local Similarity 81.7%; Pred. No. 1.9e-205;
 Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;
 QY 1 ATGGCTGAGCTAGCTGACACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 60
 Db 55 ATGGCTGAGCTAGCTGACACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 114
 QY 61 AAGACCTCTCTGGGACCAAGCTGGAAGCAAGTACCTGTGCTCCGCTGAGAAAGTC 120
 Db 115 AAGACCTCTCTGGGACCAAGCTGGAAGCAAGTACCTGTGCTCCGCTGAGAAAGTC 174
 QY 121 CTCGCAGGCCCTTCCAGGCGCAGTGGGCCACCGGTACTGCTCTCTGCTGCGCCAGC 180
 Db 175 CTCGCAGGCCCTTCCAGGCGCAGTGGGCCACCGGTACTGCTCTCTGCTGCGCCAGC 234
 QY 181 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTTACGAGGCGATATATGAAGAA 240
 Db 235 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTTACGAGGCGATATATGAAGAA 294
 QY 241 GGCATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATATGCTGCCCGCAGGAGTG 300
 Db 295 GGCATTTCTATTTAGAAAGCAGTTCCGCTTCCAGATATGCTGCCCGCAGGAGTG 354
 QY 301 GAGAGCTGCCGCGCTGTGCTCCAGTATGATGACCTGGAAGGGGACCTGAAGAA 360
 Db 355 GAGAGCTGCCGCGCTGTGCTCCAGTATGATGACCTGGAAGGGGACCTGAAGAA 414
 QY 361 TAGG----- 364
 Db 415 TACGAGAGCTGCCAGAAAGCCGCTGCCGCTCATGCTGACCGAATGCTCCGCGTGTAAA 474
 QY 365 ----- 364
 Db 475 GGCCTGTGTCGCTTGTGTAAGAGAGCGCCACCTGGAGCAGAGTGCCTGGAGAGAAGC 534
 QY 365 ----- 364
 Db 535 CTGAGCTGCCGCGCATTCGCGGCGACCTGTGTCGAGACGACGTGAAGGGCGCACACGAG 594
 QY 365 ----- 364
 Db 595 GTCTGCCCCAAGTTCCCTTAACTTTGTGACGGCTGCGCAAGAGAAGATCCCTCCGGAG 654
 QY 365 -AGTTTCAGAGCAACGTCAGACCTTGTGGCAAGTGTGAGTCCCTTCGAGATTCACGCC 423
 Db 655 AAGTTTCAGAGCAACGTCAGACCTTGTGGCAAGTGTGAGTCCCTTCGAGATTCACGCC 714
 QY 424 ATCGGCTCCTCGAGACGCTAGAGGGTGAGAAACAGCAGGAGCAGAGGTGCGTGGCTG 483
 Db 715 ATCGGCTCCTCGAGACGCTAGAGGGTGAGAAACAGCAGGAGCAGAGGTGCGTGGCTG 774
 QY 484 CGGAGACCTTGGCCATGCTACTGAGCTCGGTGTGAGGAGGCAAGAGCCCTTGGAGAC 543
 Db 775 CGGAGACCTTGGCCATGCTACTGAGCTCGGTGTGAGGAGGCAAGAGCCCTTGGAGAC 834
 QY 544 CAGACCAAGCGGGGTGAGACCTCTCGAGAGGTGCGAGACCTTGGAGAGCAAGACCGCC 603
 Db 835 CAGACCAAGCGGGGTGAGACCTCTCGAGAGGTGCGAGACCTTGGAGAGCAAGACCGCC 894
 QY 604 ACTTTTGAAGCAATTTGCTGCGTCTGAAACCGGAGGTGGAGAGGGTGGCCATCACTGCC 663
 Db 895 ACTTTTGAAGCAATTTGCTGCGTCTGAAACCGGAGGTGGAGAGGGTGGCCATCACTGCC 954
 QY 664 GAGGCTCTGACCGGCGCAGCACCCTGAGCAAGCAAGATTGAAGCCCTGAGTAGCAAG 723
 Db 955 GAGGCTCTGACCGGCGCAGCACCCTGAGCAAGCAAGATTGAAGCCCTGAGTAGCAAG 1014
 QY 724 GTGACAGAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGCGATGGCTGACTTGGAGCAG 783
 Db 1015 GTGACAGAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGCGATGGCTGACTTGGAGCAG 1074
 QY 784 AAGGCTTTGGAGATGGAGGCGATCCACCTACGATGGGTCTTCTATCTGGAAGATCTCAGAC 843

Db 1075 AAGGTGAGCCCTTCCAGCGGAGTGTGGCCACCGGTACTGCTCTTCTGCTGCGCCAGC 1134

Qy 844 TTGCGCAGAAAGCTCCAGGAAGCTGTGGTGCCGCATACCGCCGATCTTCTCCCGACCC 903

Db 1135 ATCCTCAGGAAGCTCCAGGAAGCTGTGGTGCCGCATACCGCCGATCTTCTCCCGACCC 1194

Qy 904 TTCTACACAGCAGGTACGGCTACAGATGTCTGCGTATCTACTGACGGGACCGC 963

Db 1195 TTCTACACAGCAGGTACGGCTACAGATGTCTGCGTATCTACTGACGGGACCGC 1254

Qy 964 ACCGGCGAGGAACACACCTGTCCCTCTTCTTTTGTGTGATGAAGGGCCGGAATGACGCC 1023

Db 1255 ACCGGCGAGGAACACACCTGTCCCTCTTCTTTTGTGTGATGAAGGGCCGGAATGACGCC 1314

Qy 1024 CTGCTGCGGTGCGCTTCAACAGAGGTGACCTTAATGCTGCTGACAGATTAACCGG 1083

Db 1315 CTGCTGCGGTGCGCTTCAACAGAGGTGACCTTAATGCTGCTGACAGATTAACCGG 1374

Qy 1084 GAGCAGCTGATTGAGCCCTTTCAGGCGCCGACGTGACTTCATCTCTTTTCAGAGGCGAGTC 1143

Db 1375 GAGCAGCTGATTGAGCCCTTTCAGGCGCCGACGTGACTTCATCTCTTTTCAGAGGCGAGTC 1434

Qy 1144 AACGACATGAACATCGCAAGCGGCTGCGCCCTCTTCTGCGCGTCTCAAGATGAGGCA 1203

Db 1435 AACGACATGAACATCGCAAGCGGCTGCGCCCTCTTCTGCGCGTCTCAAGATGAGGCA 1494

Qy 1204 AAGATTCTCTAGTGGGAGCATGCCATCTTTCATCAAGGCGCATGTGACCTGACAGGG 1263

Db 1495 AAGATTCTCTAGTGGGAGCATGCCATCTTTCATCAAGGCGCATGTGACCTGACAGGG 1554

Qy 1264 CTCTAA 1269

Db 1555 CTCTAA 1560

RESULT 6

AD001949

ID AAD01949 standard; cDNA; 2262 BP.

XX

AC AAD01949;

DT

XX

26-MAR-2001 (first entry)

XX

DE Human TNF-receptor associated factor (TRAF2) cDNA.

XX

Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;

KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;

KW TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; cardiac; vasotropic;

KW antipsoriatic; antineumatic; antiarthritic; antidiabetic;

KW antiatherosclerotic; immunosuppressive; Crohn's disease; psoriasis;

KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;

KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;

KW neurodegenerative disease; ss.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT Location/Qualifiers

FT 55..1560

FT /tag= a

FT /product= "Human TRAF2 protein"

FT 58..315

FT misc_feature

FT /tag= b

FT /note= "This region is truncated in TRAF2TD nucleic acid

FT sequence"

FT 421..657

FT misc_feature

FT /tag= c

FT /note= "This region is truncated both in TRAF2TR and

FT TRAF2TD nucleic acid sequences"

XX

WO200066737-A1.

PN

XX

09-NOV-2000.

PD

XX

PF 06-APR-2000; 2000WO-US009178.

XX

PR 30-APR-1999; 99US-0131940P.

XX

PA (AVET) AVENTIS PHARM PROD INC.

XX

PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;

XX

XX WPI; 2001-007223/01.

DR P-PSDB; AAY71903.

XX

XX New nucleic acid encoding variants of tumor necrosis factor receptor

PT associated factors useful for inhibiting tumor necrosis factor alpha-

PT regulated pathways; and for treating Crohn's disease, psoriasis, and

PT rheumatoid arthritis.

XX

FS Example 1; Fig 4a; 74pp; English.

XX

CC The present sequence is a cDNA encoding a full-length (i.e. non-spliced)

CC form of human tumour necrosis factor (TNF)-receptor associated factor

CC (TRAF2) protein (referred to in the specification as TRAF2-FL). TRAF2-FL

CC has two variants, a splice variant of TRAF2 referred as "TRAF2 truncated"

CC (TRAF2TR) and a TRAF2 expression construct with enhanced dominant

CC negative properties referred as "TRAF2 truncated-deleted" (TRAF2TD).

CC TRAF2-TR and TRAF2-TD are capable of inhibiting TNF alpha signalling

CC pathways. TRAF2 variants are useful for inhibiting diseases involving

CC over production of TNFalpha, TNFalpha pathologies involving

CC hyperactivation of nuclear factor kappa B (NFkB). The variants are also

CC useful for inhibiting and treating inflammatory processes involving

CC TNFalpha such as Crohn's disease, psoriasis, rheumatoid arthritis, graft

CC versus host disease, non-insulin dependent diabetes, inflammatory bowel

CC disease, and neurodegenerative diseases or cardiovascular disease such as

CC cardiac ischaemia-reperfusion injury following myocardial infarction.

CC coronary artery bypass surgery, cardiac transplantation or ischaemia-

CC reperfusion injury in the central nervous system (CNS) following stroke,

CC the progression and rupture of advanced coronary atherosclerotic plaques,

CC development and progression of congestive heart failure, endothelial cell

CC injury following balloon angioplasty, or apoptotic cell death of

CC myocardial cells

XX

SQ Sequence 2262 BP; 452 A; 664 C; 727 G; 419 T; 0 U; 0 Other;

Query Match 75.6%; Score 959.6; DB 5; Length 2262;

Best Local Similarity 81.7%; Pred. No. 1.9e-205;

Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

Qy 1 ATGCGTCAGCTAGCTGACGCCCCCTGGCTCCCTCGAGTTGCTAGACGCCGCTTCTCC 60

Db 55 ATGCGTCAGCTAGCTGACGCCCCCTGGCTCCCTCGAGTTGCTAGACGCCGCTTCTCC 114

Qy 61 AAGACCTCTCTGGGACCAAGCTGGAAGCCCAAGTACTGTCTCCGCTGCAAGAACGTC 120

Db 115 AAGACCTCTCTGGGACCAAGCTGGAAGCCCAAGTACTGTCTCCGCTGCAAGAACGTC 174

Qy 121 CTCGGAGGCGCTTCAGGCGGAGTGTGGCCACCGGTACTGCTCTCTGCTGGCGCAGC 180

Db 175 CTCGGAGGCGCTTCAGGCGGAGTGTGGCCACCGGTACTGCTCTCTGCTGGCGCAGC 234

Qy 181 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGTTCACGAGGCGCATATATGAAGAA 240

Db 235 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGTTCACGAGGCGCATATATGAAGAA 294

Qy 241 GGCATTTCATTTTAGAAGCAGTTCGGCTTCCAGATTAATCTCCGCGCAGGAGGTG 300

Db 295 GGCATTTCATTTTAGAAGCAGTTCGGCTTCCAGATTAATCTCCGCGCAGGAGGTG 354

Qy 301 GAGAGCTCGCGCGCTCTGTCTCCAGTGTGATGACCTGGAAGGGGACCCCTGAAGAA 360

Db 355 GAGAGCTCGCGCGCTCTGTCTCCAGTGTGATGACCTGGAAGGGGACCCCTGAAGAA 414

Qy 361 TACG-----

Db 415 TACGAGAGCTGCCAAGGCGCGCTGCCGCTCATGTGACCGAATGTCCTCCGCTGTAAA 474

QY 365 ----- 364
 Db 475 GGCCTGGTCCGCTTGGTAAAGAGGCGCCACCTGGAGCAGAGTGCCTCCGAGAGAGC 534
 QY 365 ----- 364
 Db 535 CTGAGCTCCGCGCATTCGCGGCAACCTGCTGCGAGCAGACGTGAAGGCGCACCCAGAG 594
 QY 365 ----- 364
 Db 595 GTCTGCCCAAGTTCCCTTAACTTTGTGACGGCTGGCGCAAGAAAGATCCCCCGGAG 654
 QY 365 - AGTTTCAGGACCAAGTCAAGACTTTGGCAAGTGTGCGAGTTCCTTGCAGATTCACGCG 423
 Db 655 AAGTTTCAGGACCAAGTCAAGACTTTGGCAAGTGTGCGAGTTCCTTGCAGATTCACGCG 714
 QY 424 ATCGCTGCTCGAGACGGTAGAGGTTGAGAAACAGCAGAGCAGAGGTGCGAGTGGCTG 493
 Db 715 ATCGCTGCTCGAGACGGTAGAGGTTGAGAAACAGCAGAGCAGAGGTGCGAGTGGCTG 774
 QY 484 CGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGAGGCAAGCCCTCTTTGGGAGAC 543
 Db 775 CGGAGCACCTGGCCATGCTACTGAGCTCGGTGCTGAGGCAAGCCCTCTTTGGGAGAC 834
 QY 544 CAGAGCCACGCGGGTTCAGAGCTCTCTGAGAGTTCGAGAGCCTTGAGAAAGAGACGGCC 603
 Db 835 CAGAGCCACGCGGGTTCAGAGCTCTCTGAGAGTTCGAGAGCCTTGAGAAAGAGACGGCC 894
 QY 604 ACTTTTGAGAACATTTGCTGCTGCTCAACCGGAGGTGAGAGGTGGCCATGACTGCC 663
 Db 895 ACTTTTGAGAACATTTGCTGCTGCTCAACCGGAGGTGAGAGGTGGCCATGACTGCC 954
 QY 664 GAGCCTTCGACCCGCGACGACCGGCTCGACCAAGATTTGAAGCCTTGAGTAGCAAG 723
 Db 955 GAGCCTTCGACCCGCGACGACCGGCTCGACCAAGATTTGAAGCCTTGAGTAGCAAG 1014
 QY 724 GTGAGCAGCTGGAGAGGAGCATTGGCTCAAGACCTGGAGCTGGAGTGGAGCAG 783
 Db 1015 GTGAGCAGCTGGAGAGGAGCATTGGCTCAAGACCTGGAGCTGGAGTGGAGCAG 1074
 QY 784 AAGTCTTTGAGATGGAGGATCCACCTAGATGGGCTTTCTATCTGGAAGATCTCAGAC 843
 Db 1075 AAGTCTAGGCTTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGGCCAGC 1134
 QY 844 TTCGCCAGGAGCTCCAGGAGCTGTGGCTGGCGGATACCGGCCATCTTCTCCCGAGCC 903
 Db 1135 ATCTCAGGAAGCTCCAGGAAGCTGTGGCTGGCGGATACCGGCCATCTTCTCCCGAGCC 1194
 QY 904 TTCTACACCAAGAGTACGGCTACAAGATGTCTGCGGTATCTACCTGAACGCGGACGGC 963
 Db 1195 TTCTACACCAAGAGTACGGCTACAAGATGTCTGCGGTATCTACCTGAACGCGGACGGC 1254
 QY 964 ACCGGGAGGAAACACCTTCTTCTGTTGTGATGAAGGCGCCGGAATGACGCC 1023
 Db 1255 ACCGGGAGGAAACACCTTCTTCTGTTGTGATGAAGGCGCCGGAATGACGCC 1314
 QY 1024 CTGCTGGGCTGGCCCTTCAACCAAGGTGACCTTAATGCTGCTGACACAGATAACCGG 1083
 Db 1315 CTGCTGGGCTGGCCCTTCAACCAAGGTGACCTTAATGCTGCTGACACAGATAACCGG 1374
 QY 1084 GAGCAGTGTATGAGCTTTAGGCGGCTGGCCCTTCTTCTGCGGCTGCTCCAGATGGAGGA 1203
 Db 1435 AAGCAGATGACATCGCAAGCGGCTGGCCCTTCTTCTGCGGCTGCTCCAGATGGAGGA 1494
 QY 1204 AAGATTCCTACGTGCGGAGGATGCCATCTTTCATCAAGGCCATTGTGGACCTGACAGGG 1263
 Db 1495 AAGATTCCTACGTGCGGAGGATGCCATCTTTCATCAAGGCCATTGTGGACCTGACAGGG 1554

QY 1264 CTCTAA 1269
 Db 1555 CTCTAA 1560
 RESULT 7
 ID ABL65876
 XX ABL65876 standard; DNA; 2262 BP.
 AC ABL65876;
 XX 15-MAY-2002 (first entry)
 DT 15-MAY-2002 (first entry)
 DE Lung cancer related gene sequence SEQ ID NO:4213.
 XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; Gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX Homo sapiens.
 OS WO200194629-A2.
 PN 13-DEC-2001.
 PD 30-MAY-2001; 2001WO-US010838.
 PF 05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0233133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 22-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 25-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 26-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 27-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.
 PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX (AVAL-) AVALON PHARM.
 PA

Query Match	75.6%	Score	959.6	DB	9	Length	2262
Best Local Similarity	81.7%	Pred. No.	1.9e-205				
Matches	1230	Conservative	0	Mismatches	39	Indels	237
Gaps	1						

Qy	1	ATGGCTCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC	60
Db	55	ATGGCTCAGCTAGCGTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC	114
Qy	61	AAGACCCCTCTGGGGACCAAGCTGGAAAGCCAAAGTACCTGTCTCCGCTCGAAGAACGTC	120
Db	115	AAGACCCCTCTGGGGACCAAGCTGGAAAGCCAAAGTACCTGTCTCCGCTCGAAGAACGTC	174
Qy	121	CTCCGAGGCCCTTCAGAGCGCAGTGGCCACCGGTACTGCTCTCTGCTGGCCAGC	180
Db	175	CTCCGAGGCCCTTCAGAGCGCAGTGGCCACCGGTACTGCTCTCTGCTGGCCAGC	234
Qy	181	ATCCTCAGCTCTGGGCCCTCAGAACTGTGCTGCTGTGTTCAAGGAGCATATATGAAGAA	240
Db	235	ATCCTCAGCTCTGGGCCCTCAGAACTGTGCTGCTGTGTTCAAGGAGCATATATGAAGAA	294
Qy	241	GGCATTTCTATTAGAAAGCAGTTCCGCTTCCAGATAATGCTGCTCCCGCAGGAGGTG	300
Db	295	GGCATTTCTATTAGAAAGCAGTTCCGCTTCCAGATAATGCTGCTCCCGCAGGAGGTG	354
Qy	301	GAGAGCCTCGCGGCGCTGTGTCCAGTGTATGATGACCTGGAAAGGGAACCTTGAAAGAA	360
Db	355	GAGAGCCTCGCGGCGCTGTGTCCAGTGTATGATGACCTGGAAAGGGAACCTTGAAAGAA	414
Qy	361	TACG-----	364
Db	415	TACGAGAGCTGCCACGAAGGCCGCTGCCGCTCATGTGACCGGAATGTCCGGGTGTAAA	474
Qy	365	-----	364
Db	475	GGCCTGTGTCGCTTGTGTGAAAGAGAGGGCCACTGTGAGCAGCAGTGCCTGGAGAGAC	534
Qy	365	-----	364
Db	535	CTGAGCTCGCGCATTCGCGGCCACCTGTCTCGGAGCAGACGTCGAAGCGCACACGAG	594
Qy	365	-----	364
Db	595	GTCTGCCCCCAAGTTCCCTTAACTTGTGAACGCTGCGGCAAGAAAGATATCCCTCCGGAG	654
Qy	365	-AGTTTCAGGACCAAGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTGACAGATTCACGCC	423
Db	655	AAGTTTCAGGACCAAGCTCAAGACTTGTGGCAAGTGTGAGTCCCTTGACAGATTCACGCC	714
Qy	424	ATCGCTGCCCTCGAGACGGTATAGAGGTGAGAAAACAGCAGGAGCAGAGTGCAGTGGCTG	483
Db	715	ATCGCTGCCCTCGAGACGGTATAGAGGTGAGAAAACAGCAGGAGCAGAGTGCAGTGGCTG	774
Qy	484	CGGAGACACCTGGCCATCTACTCAGCTCGGTGTGTGGAGGCAAGGCCCTCTTGGAGAC	543
Db	775	CGGAGACACCTGGCCATCTACTCAGCTCGGTGTGTGGAGGCAAGGCCCTCTTGGAGAC	834
Qy	544	CAGAGCCACGCGGGTTCAGAGCTCCTCGAGAGGTTCGAGAGCCTTGAGAGAAAGACGCC	603
Db	835	CAGAGCCACGCGGGTTCAGAGCTCCTCGAGAGGTTCGAGAGCCTTGAGAGAAAGACGCC	894
Qy	604	ACTTTTGAAGACATTGTCTGGTCTCTGAAACCGGAGGTGGAGAGGTGGCCATGACTGCC	663
Db	895	ACTTTTGAAGACATTGTCTGGTCTCTGAAACCGGAGGTGGAGAGGTGGCCATGACTGCC	954
Qy	664	GAGGCTCGAGCCGSCAGCACCGGCTGGACCAAGATTTGAAGCCCTGAGTAGCAAG	723
Db	955	GAGGCTCGAGCCGSCAGCACCGGCTGGACCAAGATTTGAAGCCCTGAGTAGCAAG	1014
Qy	724	GTGAGCAGCTGGAGAGGAGCATTGGCCCTCAGGACCTGGCGATGGCTGACTTGGAGCAG	783
Db	1015	GTGAGCAGCTGGAGAGGAGCATTGGCCCTCAGGACCTGGCGATGGCTGACTTGGAGCAG	1074
Qy	784	AAGGCTCTTGGAGATGGAGGCGATCCACCTACGATGGGGTCTTTCATCTGGAAGATCTCAGAC	843

PT which the gene is involved, or as target molecules for gene therapy.

XX Claim 1; SEQ ID NO 63; 205pp; English.

XX The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA5710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 2094 BP; 419 A; 610 C; 661 G; 404 T; 0 U; 0 Other;

Query Match 67.4%; Score 855.6; DB 10; Length 2094;
Best Local Similarity 81.5%; Pred. No. 4.1e-182;
Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6;

QY 1 ATGGCTGAGCTAGCGTACACCCCTCCCTGGCTGCTGAGTGTCTACAGCCGGCTTCTCC 60
DB 45 ATGGCTGAGCTAGCGTACACCCCTCCCTGGCTGCTGAGTGTCTACAGCCGGCTTCTCC 104
QY 51 AAGACCTCTCTGGGACCAAGCTGGAAGCCAAAGTACCTGCTCCGCTGCGAGAAAGTTC 120
DB 105 AAGACCTCTCTGGGACCAAGCTGGAAGCCAAAGTACCTGCTCCGCTGCGAGAAAGTTC 164
QY 121 CTCCGAGCCCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGCTGGCCAGC 180
DB 165 CTCCGAGCCCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGCTGGCCAGC 224
QY 181 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 225 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
QY 241 GGCATTTCTATTAGAAAGCAGTTCGGCTTCCAGTAATGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 285 GGCATTTCTATTAGAAAGCAGTTCGGCTTCCAGTAATGCTGCTGCTGCTGCTGCTGCTGCT 344
QY 301 GAGAGCTTCCGCGCTGTGCTCCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 360
DB 345 GAGAGCTTCCGCGCTGTGCTCCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 404
QY 361 TACGAGTTCA -----GACACAGCTCAAGACTTGTGCAAGTGTGCAAGTGTGCAAGT 409
DB 405 TACGAGTTCAAGTGTGCGTGTGCGATGCTGACAGAGCTCCAGCAGTCTGCGAGTCTGCT 464
QY 410 GCAGATTTCCAC -----GCCATCGGC 429
DB 465 CCAGCTTCCCAAGCAGTTATGACCTTGTCTGACGTTCTCTACTGGGCTGAGCC 524
QY 430 TGCCTCAGACGGTGAAGGTGAGAAACAGAG -----GAGCAGAGGTGCAAGTGTGCTGC 484
DB 525 TGTCTGATGTGTGAGAGGAGAGACAGGAGTGTCTCTAGAGCTGCCACGAGGCGCG 584
QY 485 GGGAGCACCTGGCCATCTACTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
DB 585 TGCCCGCTCATGTGACCGATGTCCCGCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
QY 544 CAGAGCCACCGGGTCTCAGAGCTCTCTCAGAGTGTGCGAGAGCTGAGAGAGAGAGAGAG 603
DB 645 GAGCGCCACCTGGAGCAGAGTGTCCCGGAGAGAGCTGAGCTGCTGCTGCTGCTGCTGCTG 704
QY 604 ACTTTTGAGAACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 705 CCTGTGCGGAGCAGACGTGAAGCGGCGACACAGAGTGTGCCCCAAGTGTCCCTTAATCT 764
QY 661 GCGAGGCTCGCAG -----CCGCGAGCAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
DB 765 TGTGACGGCTGCGCAAGAGAGATATCCCGGAGAGAGTTTTCAGACCAAGCAGAGATT 824
QY 706 GAGCCCTGAGTACAGAGTGTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 765
DB 825 GAGCCCTGAGTACAGAGTGTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 884
QY 766 ATGGCTGACTTGGAGCAGAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGCTCTTC 825

DB 885 ATGGCTGACTTGGAGCAGAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGCTCTTC 944
QY 826 ATCTGGAAGATCTCAGACTTCCCGAGGAGCTCCAGGAGAGCTGTGCTGGCGGATATACC 885
DB 945 ATCTGGAAGATCTCAGACTTCCCGAGGAGAGCTCCAGGAGAGCTGTGCTGGCGGATATACC 1004
QY 886 GGCATCTTCTCCCGAGCTTCTACACCGAGGAGCTACGAGTGTGCTGCTGCTGCTGCTGCT 945
DB 1005 GGCATCTTCTCCCGAGCTTCTACACCGAGGAGCTACGAGTGTGCTGCTGCTGCTGCTGCT 1064
QY 946 TACCTGAGCGGAGGAGGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1005
DB 1065 TACCTGAGCGGAGGAGGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1124
QY 1006 AAGGGCCCGAATGAGCGCTGCTGCGGTGGCCCTTCAACCGAGAGGAGGAGGAGGAGGAGG 1065
DB 1125 AAGGGCCCGAATGAGCGCTGCTGCGGTGGCCCTTCAACCGAGAGGAGGAGGAGGAGGAGG 1184
QY 1066 CTCGACCGAGATTAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1125
DB 1185 CTCGACCGAGATTAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1244
QY 1126 TCTTTTCAGAGGCGGAGTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1185
DB 1245 TCTTTTCAGAGGCGGAGTCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1304
QY 1186 GTCTCAAGATGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1245
DB 1305 GTCTCAAGATGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1364
QY 1246 ATTGTGCGACCTGACAGGCGCTCTAA 1269
DB 1365 ATTGTGCGACCTGACAGGCGCTCTAA 1388

RESULT 12

ABI99821
ID ABI99821 standard; cDNA; 2121 BP.

XX AC ABI99821;

XX DT 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:935.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX OS Mus musculus.

XX PN W0200188188-A2.

XX PD 22-NOV-2001.

XX PF 18-MAY-2001; 2001WO-JP004192.

XX PR 18-MAY-2000; 2000JP-00145977.

XX PA (UNYI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX DR WPI; 2002-034733/04.

XX DR P-PSDB; ABB57335.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
XX genes.

XX PS Claim 2; Page 2360-2364; 2690pp; English.

XX DE Human adipocyte Selected Interacting domain, SID, cDNA #415.
 XX DE Human, ss; gene, prey; adipocyte; SID; selected interacting domain;
 XX DE anorectic; antidiabetic; protein-protein interaction; diabetes;
 XX DE yeast 2-hybrid assay; metabolic disorder; obesity.
 XX OS Homo sapiens.
 XX PN WO200286122-A2.
 XX PD 31-OCT-2002.
 XX PF 14-MAR-2002; 2002WO-EF003768.
 XX PR 14-MAR-2001; 2001US-0275734P.
 XX PA (HYBR-) HYBRIGENICS.
 XX PI Legrain P, Daviet L;
 XX WI 2003-103412/09.
 XX DR P-PSDB; ABU70784.
 XX PT New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 PT obesity or diabetes.
 XX PS Claim 7; Page 249; 382pp; English.
 XX CC The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (RTM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a
 CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (RTM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence encodes a SID
 CC (prey) protein of the invention
 XX SQ Sequence 979 BP; 215 A; 286 C; 291 G; 187 T; 0 U; 0 Other;
 Query Match 45.9%; Score 582.2; DB 8; Length 979;
 Best Local Similarity 98.7%; Pred. No. 7.8e-121;
 Matches 587; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 675 CCGGACGACCGGTGACCAAGACGATTTGAAGCCCTGAGTAGCAAGGTGACGAGCT 734
 DB 385 CCGGAGAGATTTTCAGGACCAAGACGATTTGAAGCCCTGAGTAGCAAGGTGACGAGCT 444
 QY 735 GGAGAGGAGCATTTGGCTCAAGACCTGGCGATGGCTTGGACGACGATCTTGA 794
 DB 445 GGAGAGGAGCATTTGGCTCAAGACCTGGCGATGGCTTGGACGACGATCTTGA 504
 QY 795 GATGAGGACATCCACCTACGATGGGTCTTCACTGGAAGATCTCAGACTTCGCCAGGAA 854
 DB 505 GATGAGGACATCCACCTACGATGGGTCTTCACTGGAAGATCTCAGACTTCGCCAGGAA 564

QY 855 GCTCCAGGAGCTGTGGTGGCCGATACCGCCGATCTTCCCGAGCCTTCTACACGAG 914
 DB 565 CCGGACGAGAGCTGTGGTGGCCGATACCGCCGATCTTCCCGAGCCTTCTACACGAG 624
 QY 915 CAGGTACGGCTACAGAGATGTGTGCGTATCTACTGACGCGGACCGGCGGAGG 974
 DB 625 CAGGTACGGCTACAGAGATGTGTGCGTATCTACTGACGCGGACCGGCGGAGG 684
 QY 975 AACACACCTGTCCCTCTTCTTTGTGGTGAAGAGGCGCGAATGACGCCCTGCTGCGGTG 1034
 DB 685 AACACACCTGTCCCTCTTCTTTGTGGTGAAGAGGCGCGAATGACGCCCTGCTGCGGTG 744
 QY 1035 GCCCTTCAACAGAGGTGACCTTAATGCTGCTCGACAGATTAACCGGAGGACGCTGAT 1094
 DB 745 GCCCTTCAACAGAGGTGACCTTAATGCTGCTCGACAGATTAACCGGAGGACGCTGAT 804
 QY 1095 TGAGCCCTTCAGGCGCGGACGTGACTTCATCTCTTTTCAGAGGCGGACGATCAACGACATGAA 1154
 DB 805 TGAGCCCTTCAGGCGCGGACGTGACTTCATCTCTTTTCAGAGGCGGACGATCAACGACATGAA 864
 QY 1155 CATGCGGAGCGGTGCGCCCTCTTCTGCGCGCTCCAAAGATGAGGCAAGAAATTCCTA 1214
 DB 865 CATGCGGAGCGGTGCGCCCTCTTCTGCGCGCTCCAAAGATGAGGCAAGAAATTCCTA 924
 QY 1215 CGTGGGAGCGATGCGCATCTTTCATCAAGGCCATTTGAGACCTGACAGGCTCTAA 1269
 DB 925 CGTGGGAGCGATGCGCATCTTTCATCAAGGCCATTTGAGACCTGACAGGCTCTAA 979

RESULT 15
 AAT31274
 ID AAT31274 standard; DNA; 2380 BP.
 XX AAT31274;
 AC AAT31274;
 XX 23-OCT-1996 (first entry)
 DE Epstein-Barr induced protein EB16 gene.
 KW EB16; Epstein-Barr induced protein 6; LAP1; LMP1 associated protein 1;
 KW latent infection membrane protein;
 KW tumour necrosis factor receptor associated factor; TRAF;
 KW signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AIDS;
 KW Hodgkin's disease; Burkitt's lymphoma; nasopharyngeal carcinoma;
 KW mononucleosis; Epstein-Barr virus; EBV; gene therapy; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 76..1326
 FT /*tag= a
 XX WO9620723-A1.
 XX PD 11-JUL-1996.
 XX 28-DEC-1995; 95WO-US016980.
 XX 30-DEC-1994; 94US-00367540.
 XX (BGM) BRIGHAM & WOMENS HOSPITAL.
 XX (REGC) UNIV CALIFORNIA.
 XX Kieff E, Mosialos G, Birkenbach M, Vanarsdale T, Ware C, Kaye KM;
 DR WPI; 1996-333765/33.
 DR P-PSDB; AAW03147.
 XX Compounds and methods for controlling TRAF-mediated signals - by
 PT modulating interactions between Epstein Barr virus encoded proteins LMP1,
 PT LAP1, TNF, TNFR to inhibit lymphoblast growth and tumorigenesis.
 XX Example 1; Page 61-63; 87pp; English.

Result No.	Score	Query Match	Length	DB	ID	Description
1	959.6	75.6	2262	3	US-09-167-109-2	Sequence 2, Appli
2	701	55.2	2121	1	US-08-331-394-3	Sequence 3, Appli
3	701	55.2	2121	1	US-08-250-858-3	Sequence 3, Appli
4	701	55.2	2121	1	US-08-446-915-3	Sequence 3, Appli
5	701	55.2	2121	1	US-08-744-139-3	Sequence 3, Appli
6	701	55.2	2121	1	US-08-779-599-3	Sequence 3, Appli
7	701	55.2	2121	5	PCR-US95-06639-3	Sequence 3, Appli
8	296.6	23.4	2380	3	US-09-167-109-1	Sequence 1, Appli
9	296.6	23.4	2380	5	PCR-US95-16980-2	Sequence 2, Appli
10	276.8	21.8	2361	3	US-08-705-771-7	Sequence 7, Appli
11	276.8	21.8	2361	4	US-09-417-540-7	Sequence 7, Appli
12	272	21.4	2088	1	US-08-331-394-1	Sequence 1, Appli
13	272	21.4	2088	1	US-08-250-858-1	Sequence 1, Appli
14	272	21.4	2088	2	US-08-446-915-1	Sequence 1, Appli
15	272	21.4	2088	2	US-08-744-139-1	Sequence 1, Appli
16	272	21.4	2088	4	US-08-779-599-1	Sequence 1, Appli
17	272	21.4	2088	5	PCR-US95-06639-1	Sequence 1, Appli
18	171.6	13.5	2894	3	US-09-138-277C-4	Sequence 4, Appli
19	171.6	13.5	2893	3	US-09-167-109-5	Sequence 5, Appli
20	165.8	13.1	2354	4	US-09-138-277C-2	Sequence 2, Appli
21	146.6	11.6	2240	3	US-08-697-610-1	Sequence 1, Appli
22	146.6	11.6	2240	3	US-08-349-357-1	Sequence 1, Appli
23	146.6	11.6	2339	4	US-09-645-926A-6	Sequence 6, Appli
24	146.6	11.6	2359	5	PCR-US95-16980-1	Sequence 1, Appli
25	145.2	11.4	1793	4	US-09-268-544B-37	Sequence 37, Appli
26	145	11.4	2455	3	US-09-167-109-3	Sequence 3, Appli
27	143.4	11.3	2065	4	US-09-268-544B-35	Sequence 35, Appli

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2121 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear

US-08-744-139-3

Query Match 55.2%; Score 701; DB 2; Length 2121;
 Best Local Similarity 71.0%; Pred. No. 2e-164;
 Matches 1068; Conservative 0; Mismatches 200; Indels 237; Gaps 1;

QY 1 ATGGCTGAGTGGTACCCCTGGCTGCTGAGTGTGTACAGCCGGCTTCTCC 60
 DB 48 ATGGCTGAGGAGTGTGACTTCCCTGGCTGCTGAGTGTGTACAGCCGGCTTCTCC 107
 QY 61 AAGACCTCTGGGGACCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGCAGAAAGTC 120
 DB 108 AAGACCTCTCTGGGGACCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGCAGAAAGTC 167
 QY 121 CTCGGCAGCCCTTCCAGCGCAGTGTGGCCACCGGTACTGCTCTTCTGCTGGCCAGC 180
 DB 168 CTGGGAGGCTTCCAGCGCCAGTGTGGCCACCGGTACTGCTCTTCTGCTGGCCAGC 227
 QY 181 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGTGTACAGGGCATATAGAAGAA 240
 DB 228 ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGTGTATGAAGGCTGTATGAAGAA 287
 QY 241 GGCATTTCTATTAGAAAGCAGTTCGGCCCTTCCAGATAATGCTGCGCCGAGGAGGTG 300
 DB 288 GGCATTTCTATTAGAGAGTGTGCTGCTGCTTCCAGATAATGCTGCGCCGAGGAGGTG 347
 QY 301 GAGACCTGCGCGGCTGTGCTCCAGTGTGATGATGATGATGATGATGATGATGATGATG 360
 DB 348 GAGACCTGCGCGGCTGTGCTCCAGTGTGATGATGATGATGATGATGATGATGATGATG 407
 QY 361 TAGCA----- 365
 DB 408 TAGGAGCTGCCAGAAAGACTTTGGCCCTTCTGCTGAGGAGTGTCTGCTGATGATAA 467
 QY 366----- 365
 DB 468 GGCCTGTGCGCTCAGCGAGAGAGGACCACTGAGCAGGAATGCCCAAGAGAGC 527
 QY 366----- 365
 DB 528 CTGAGCTGCCAGACTGCGAGAGCCCTGTGTAGCAGCTGAGAGTGTACATATGAG 587
 QY 366----- 365
 DB 588 GTCTGCCCCNAGTTTCCCTTAACCTGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTG 647
 QY 366---GTTTTCAGGACCACTGCAAGCTGTGCGAAGTGTGAGTCCCTTCCAGATTCACGCC 423
 DB 648 ACCTTTTCAGGACCACTGTTAGAGCTGTGAGCAATGCGCGGTCTCTCAGATTTCCACCC 707
 QY 424 ATCGCTCTCTCGAGACGGTGTGAGGTTGAGAAACAGCAGGAGACGAGGTGCGATGCTG 483
 DB 708 GTTGGCTGTTTTCAGAGTGTGAGAGTGTGAGAACTGTGAGAGTGTGAGAGTGTGAG 767
 QY 484 CGGAGACCTTGGCATGCTACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
 DB 768 CGGAGACCACTTGGCATGCTACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 827
 QY 544 CAGACCACTGCGGCTGAGCTCTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
 DB 828 TTGAACCACTGCGGCTGAGCTTCTCAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 887
 QY 604 ACTTTTGAACAATTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
 DB 888 ACCTTTGAACAATTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 947
 QY 664 GAGCCTGACCCGGCAGCAGCCGCTGAGCAAGCAAGATTGAGCCCTGAGTAGCAAG 723

DB 948 GAGGCTTGTAGCCGCGCAGCAGCCGCTAGACAGGACAAAGATTGAGCCCTGAGTAAACAG 1007
 QY 724 GTGACAGCTGTGAGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAG 783
 DB 1008 GTGCAACAGCTGTGAGAGGAGCATCGGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAG 1067
 QY 784 AAGGCTCTTGGAGATGGAGGAGCATCCACTACGATGGGGTCTTTCATCTGGAAGATCTCAGAC 843
 DB 1068 AAGGCTCTCGAGTTCGAAAGTATCCACCTATGATGGGTCTTTCATCTGGAAGATCTCAGAC 1127
 QY 844 TTGCGCAGGAAGCTCCAGGAAGCTGTGCTGCGCCGATACCCGCTATCTTCTCCCGAGCC 903
 DB 1128 TTCAACAGAAAGCTGTCAGGAAGCTGTGCTGCGCCGATACCCGCTATCTTCTCCCGAGCC 1187
 QY 904 TTCTACACAGCAGGTAGCGGTACAAAGATGTCTGCGTATCTACCTGAACGGGACGGC 963
 DB 1188 TTCTACACAGCAGGTAGCGGTACAAAGATGTCTGCGTATCTACCTGAACGGGACGGC 1247
 QY 964 ACCGGCAGGAAGAACACCTGTCTCTTCTTGTGCTGATGAAGGCGCCGAAATGACGCC 1023
 DB 1248 ACTGGCGCGGAACTCATCTGTCTCTTCTTGTGCTGATGAAGGCGCCCAATGATGCT 1307
 QY 1024 CTGCTGCGGTGCGCTTCAACAGGAAGTGAACCTTAATGCTGCTGACCAAGAAACCGG 1083
 DB 1308 CTGTTGCAAGTGGCTTTAATCAGAAAGTAACTGATGTTGCTGGACCATAAACCGG 1367
 QY 1084 GAGCAGCTGATTGAGCGCTTTCAGGCGCCGACGTGCTTCTCTCTTTCAGAGGCGAGTC 1143
 DB 1368 GAGCATGTGATCGACGCTTTCAGGCGCCGATGATGATGATGATGATGATGATGATG 1427
 QY 1144 AACGACATGAACATCGAAGCGCTGCGCCCTCTTCTGCGCCGCTTCTTCTTCTTCTTCT 1203
 DB 1428 AATGACATGAACATCGAAGCGCTGCGCCCTCTTCTGCGCCCTCTTCTTCTTCTTCTTCT 1487
 QY 1204 AAGAAATTCCTAGTGGGAGCAGTCCCATCTTTCATCAAGGCGCATTTGGACCTGACAGG 1263
 DB 1488 AAGAAATTCCTAGTGGGAGCAGTCCCATCTTTCATCAAGGCGCATTTGGACCTGACAGG 1547
 QY 1264 CTCTA 1268
 DB 1548 CTCTA 1552

RESULT 6

US-08-779-599-3
 ; Sequence 3, Application US/08779599
 ; Patent No. 6500922
 ; GENERAL INFORMATION:
 ; APPLICANT: Goeddel, David V.
 ; APPLICANT: Rothe, Mike
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/779,599
 ; FILING DATE: 07-Jan-1997
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: P0897C2

; PILING DATE: 27-MAY-1994		; DB 5; Length 2121;	
; PRIOR APPLICATION DATA: 08/331394		; Best Local Similarity 71.0%; Pred. No. 2e-164;	
; FILING DATE: 28-OCT-1994		; Matches 1068; Conservative 0; Mismatches 200; Indels 237; Gaps 1;	
; ATTORNEY/AGENT INFORMATION:			
; NAME: Dreger, Ginger R.			
; REGISTRATION NUMBER: 33,055			
; REFERENCE/DOCKET NUMBER: 897P2PCT			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 415/225-3216			
; TELEFAX: 415/952-9881			
; TELEX: 910/371-7168			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 2121 bases			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; PCT-US95-06639-3			
QY	1	ATGGCTGAGCTAGCGTACCCCGCTGGCTCCCTGAGTTGCTACAGCCGGCTTCCTCC	60
DB	48	ATGGCTGAGCTAGCGTACCCCGCTGGCTCCCTGAGTTGCTACAGCCGGCTTCCTCC	107
QY	61	AAGACCTCTCTGGGAGCAAGCTGAGCCCAAGTACCTGCTCCCGCTCCAGAAAGTC	120
DB	108	AAGACCTCTCTGGGAGCAAGCTGAGCCCAAGTACCTGCTCCCGCTCCAGAAAGTC	167
QY	121	CTCCGAGCGCTCTCCAGCGCAGTGTGGCCACCGTACTGCTCTCTCTCTCTCTCTCT	180
DB	168	CTCCGAGCGCTCTCCAGCGCAGTGTGGCCACCGTACTGCTCTCTCTCTCTCTCTCT	227
QY	181	ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
DB	228	ATCTCAGCTCTGGGCTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	287
QY	241	GCCATTTCTATTAGAAAGCAGTTCGGCTCTCCAGATTAATGCTGCTGCTGCTGCTG	300
DB	288	GCCATTTCTATTAGAAAGCAGTTCGGCTCTCCAGATTAATGCTGCTGCTGCTGCTG	347
QY	301	GAGAGCTGCGCGCTGTGCTCAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
DB	348	GAGAGCTGCGCGCTGTGCTCAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	407
QY	361	TACGA-----	365
DB	408	TACGAGCTGCCAGAGGACTTTGGCCATTCTGCTGAGCGAGTGTCTGCTGCTGCTG	467
QY	366	-----	365
DB	468	GGCTGTGCTGCTCAGCGAGGAGGACCACTGAGCAGGAAATGCCCAAAAGGAGC	527
QY	366	-----	365
DB	528	CTGAGCTGCCAGCACTGAGAGCACTGTGAGCCAGTGTGAGGAGTGTGAGTGTGAG	587
QY	366	-----	365
DB	588	GTCTGCCCAAGTTTCCCTTAACCTGTGATGGCTGTGGCGAAGAAATCCCTCGGGAG	647
QY	366	-----	423
DB	648	ACGTTTCAGGACCATTTAGAGCATGAGCAATGCGCGGTTCTCTGAGATTTCCACCC	707
QY	424	ATCCGCTGCTCGAGCGGTAGAGGTTGAGAAACAGCAGGAGCAGGAGTGTGAGTGTG	483
DB	708	GTGCTGCTCGAGAGTGTGAGACTGAGAACTGAGGATCATGAGCTGAGCGGCTA	767
QY	484	CGGAGCACCTGGCCATGCTACTGAGCTCGGTGTGGAGGCAAGCCCTCTTTGGGAGAC	543

RESULT 8
 US-09-167-109-1
 ; Sequence 1, Application US/09167109
 ; Patent No. 6399297
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Cowsert, Lex M.
 ; APPLICANT: Monia, Brett P.
 ; APPLICANT: Xu, Xiaoxing S.
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
 ; FILE REFERENCE: ISPH-0321
 ; CURRENT APPLICATION NUMBER: US/09/167,109
 ; CURRENT FILING DATE: 1998-10-06
 ; NUMBER OF SEQ ID NOS: 228
 ; SEQ ID NO 1
 ; LENGTH: 2380
 ; TYPE: DNA


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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1326)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: U19261 Genbank
; DATABASE ENTRY DATE: 1995-02-21
; US-09-167-109-1

Query Match      23.4%; Score 296.6; DB 3; Length 2380;
Best Local Similarity 66.2%; Pred. No. 4.5e-64;
Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGGAGAGAGAGCGGCCACTTTTGAGAACATGTCGTCTGACCGGAGGTGGAG 645
Db      |||||
QY 643 CTGGAGGGAGAGTGGGTGTGTTGAGAACATGTTGCTCTCAACAGAGGTGGAG 702
Db      |||||
QY 646 AGGGTGGCATGATGCGCGAGGCTGACGGCGGAGCAGCGGTGGACCAAGACAAATT 705
Db      |||||
QY 703 GCCTCCACCTGGCCCTGGCCACCTCTATCCACAGAGCCAGTGGACCGGATC 762
Db      |||||
QY 706 GAAGCCTGAGTAGCAAGGTGCAGAGTGGAGAGGATGCGCTCAAGACCTGGCG 765
Db      |||||
QY 763 CTGAGCTTGGAGCAGAGGTGCGCCCTCAGAGAGGCGCTCTTCATGGCACTTC 822
Db      |||||
QY 766 ATGGCTGACTTGGAGCAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGTTC 825
Db      |||||
QY 823 CTGGCAAGCTGGAGCAGAGTTCGGCTCATGGAGGAGGCTCTTCGATGGCACTTC 882
Db      |||||
QY 826 ATCTGGAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGGTGGCGCGCATACC 885
Db      |||||
QY 883 CTGTTGAGATGACCAATGTCCAGGCGGTGCCATGAGTCGCGCTGTGGCAGGACCGTC 942
Db      |||||
QY 886 GCCATCTTCTCCCGAGCCTTCTACACCCAGCAGGTACCGCTACAGATGTGTCTCGTATC 945
Db      |||||
QY 943 AGCCTCTTCTCCCGAGCCTTCTACATGCCAAGTATGGCTACAAAGTGTGCTCGGCTG 1002
Db      |||||
QY 946 TACCTGAACGGCGAGCGGACCGGCGGAGGAACACACCTGTCTCTCTTTTGTGGTATG 1005
Db      |||||
QY 1003 TACCTGAATGGAGATGGCACTGGAAGAGAACCCATCTGTCTCTTCATCGTATCATG 1062
Db      |||||
QY 1006 AAGGCCCGGAATGAGCGCCTCTCTGGTGGCGCTTCAACAGAAAGGTGACCTTAAATGCTG 1065
Db      |||||
QY 1063 AGAGGGAGATGATGCGCTGCTGCGGTGGCGCTTCCGGAACAGGTACCTTCATGCTG 1122
Db      |||||
QY 1066 CTCGACCAAGATAACCGGGAGCAGCGTATTGACGCTTTAGGCGCTTCCAGGCGGAGTCACTTC 1125
Db      |||||
QY 1123 CTGGACCAAGAACACCGTGAGCAGCGCATTTAGCGCTTCAGGCGCGAGCTGACTTCATCC 1182
Db      |||||
QY 1126 TCTTTTTCAGAGGCGAGTCAACGACATGAACATCGAAGCGGCTGCCCTCTTCTGCCCC 1185
Db      |||||
QY 1183 TCCTTCCAGAGGCCCGCAGAGTGAAACCAAGCTGGCCAGTGGATGCCACTCTTCTTCCCC 1242
Db      |||||
QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTAGCTGGGAGCATGCCATCTTCATCAAG 1242
Db      |||||
QY 1243 CTGAGCAAACTGAGTCAACCAAGACGCGCTACGTGAAGGACACAAATGTTCTCTCAAG 1302
Db      |||||
QY 1243 GCCATTGTGGA 1253
Db      |||||
QY 1303 TGCAATTGTGA 1313
Db      |||||

RESULT 9
PCT-US95-16980-2
; Sequence 2, Application PC/TUS9516980
; GENERAL INFORMATION:
; APPLICANT: Brigham & Women's Hospital
; TITLE OF INVENTION: CONTROLLING TRAP-MEDIATED SIGNALS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston

```

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; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16980
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,540
; FILING DATE: 30-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 05311/014W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)542-5070
; TELEFAX: (617)542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2380 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 76..1323
; PCT-US95-16980-2

Query Match      23.4%; Score 296.6; DB 5; Length 2380;
Best Local Similarity 66.2%; Pred. No. 4.5e-64;
Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGAGAGAGAGAGCGGCCACTTTTGAGAACATGTCGTCTCTGAGAACCGGAGGTGGAG 645
Db      |||||
QY 643 CTGAGGGAGAGCTGCGTGTGTTGAGAACATGTTGCTCTCAACAGGAGGTGGAG 702
Db      |||||
QY 646 AGGGTGGCATGATGCGCGAGGCTGACGGCGGAGCAGCGGTGGACCAAGACAAATT 705
Db      |||||
QY 703 GCCTCCACCTGGCCCTGGCCACCTCTATCCACAGAGCCAGTGGACCGGATC 762
Db      |||||
QY 706 GAAGCCTGAGTAGCAAGGTGCAGAGTGGAGAGGATTTGGCCTCAAGACCTGGCG 765
Db      |||||
QY 763 CTGAGCTTGGAGCAGAGGTGTTGAGCTTCAGCAGACCTTGGCCCGAGAAAGACAGGCC 822
Db      |||||
QY 766 ATGGCTGACTTGGAGCAGAGTCTTGGAGATGGAGGATCCACCTACGATGGGTTC 825
Db      |||||
QY 823 CTGGCAAGCTGGAGCAGAGTTCGGCTCATGGAGGAGGCTCTTCGATGGCACTTC 882
Db      |||||
QY 826 ATCTGGAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGGTGGCGCGCATACC 885
Db      |||||
QY 883 CTGTTGAGATGACCAATGTCCAGGCGGTGCCATGAGTCGCGCTGTGGCAGGACCGTC 942
Db      |||||
QY 886 GCCATCTTCTCCCGAGCCTTCTACACCCAGCAGGTACCGCTACAGATGTGTCTCGTATC 945
Db      |||||
QY 943 AGCCTCTTCTCCCGAGCCTTCTACATGCCAAGTATGGCTACAAAGTGTGCTCGGCTG 1002
Db      |||||
QY 946 TACCTGAACGGCGAGCGGACCGGCGGAGGAACACACCTGTCTCTCTTTTGTGGTATG 1005
Db      |||||
QY 1003 TACCTGAATGGAGATGGCACTGGAAGAGAACCCATCTGTCTCTTCATCGTATCATG 1062
Db      |||||
QY 1006 AAGGCCCGGAATGAGCGCCTCTCTGGTGGCGCTTCAACAGAAAGGTGACCTTAAATGCTG 1065
Db      |||||
QY 1063 AGAGGGAGATGATGCGCTGCTGCGGTGGCGCTTCCGGAACAGGTACCTTCATGCTG 1122
Db      |||||
QY 1066 CTCGACCAAGATAACCGGGAGCAGCGTATTGACGCTTTAGGCGCTTCAGGCGCGAGCTGACTTCATCC 1125
Db      |||||
QY 1123 CTGGACCAAGAACACCGTGAGCAGCGCATTTAGCGCTTCAGGCGCGAGCTGACTTCATCC 1182
Db      |||||
QY 1126 TCTTTTTCAGAGGCGAGTCAACGACATGAACATCGAAGCGGCTGCCCTCTTCTGCCCC 1185
Db      |||||
QY 1183 TCCTTCCAGAGGCCCGCAGAGTGAAACCAAGCTGGCCAGTGGATGCCACTCTTCTTCCCC 1242
Db      |||||
QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTAGCTGGGAGCATGCCATCTTCATCAAG 1242
Db      |||||
QY 1243 CTGAGCAAACTGAGTCAACCAAGACGCGCTACGTGAAGGACACAAATGTTCTCTCAAG 1302
Db      |||||
QY 1243 GCCATTGTGGA 1253
Db      |||||
QY 1303 TGCAATTGTGA 1313
Db      |||||

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QY 1126 TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCTCTTCTGCCCC 1185
 Db 1183 TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCTCTTCTGCCCC 1242
 QY 1186 GTCTCCAGATGGAGGCA---AAGAAATTCCTACGTGCGGAGCATGCAATCTTCATCAAG 1242
 Db 1243 CTCAGCAAACTGCAGTCAACCAAGCAAGCGCTACGTGAAGGACGACACAATGTTCTCTCAAG 1302
 QY 1243 GCCATTGTGGA 1253
 Db 1303 TCATTGTGGA 1313

RESULT 10
 US-08-705-771-7
 ; Sequence 7, Application US/08705771
 ; Patent No. 6054289
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
 ; APPLICANT: Jian Ni and Jing-Shan Hu
 ; TITLE OF INVENTION: Human Genes, Sequences and
 ; TITLE OF INVENTION: Expression Products
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/705,771
 ; FILING DATE: August 30, 1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; REFERENCE/DOCKET NUMBER: 325800-346 (PFI96)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 973-994-1700
 ; TELEFAX: 973-994-1744
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2361 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-705-771-7

Query Match 21.8%; Score 276.8; DB 3; Length 2361;
 Best Local Similarity 64.3%; Pred. No. 3.7e-59;
 Matches 431; Conservative 0; Mismatches 237; Indels 2; Gaps 1;
 QY 586 CTGAGAGAGAGAGCGGCACCTTTGAGAAATGCTGTGCGTCTGCAACCGGAGGTGGAG 645
 Db 645 CTGAGAGAGAGAGCGGCCTGTGTTGAGAAATGCTGTGCGTCTGCAACCGGAGGTGGAG 704
 QY 646 AGGTGTGCGTGTGCTGCGGAGGCTGCGAGCGGCGAGCACCGGCTGGACCAAGACAGATT 705
 Db 705 GCCTCCACCTGGCCCTGGCCACCTCTATCCACGAGGACAGTGGACCGTGAAGCCATC 764
 QY 706 GAAGCCCTGAGTAGCAGGTGCGAGCACTGGAGGAGGACATTGGCTCTAAGGACCTGGCG 765
 Db 765 CTGAGCTTGGAGCAGAGGGGTGGTGCAGGTTTCAGCAGACCCCTGCGCCCAAGAACAGCAGGCC 824

QY 766 ATGGCTGACTTGGAGCAGAGGCTTTGGAGATGGAGGATCCACCTAGCATGGGGTCTTC 825
 Db 825 CTGGGCAAGCTGGAGCAGAGCTTGGCGCTCATGGAGGAGGCTCTCTTCGATGGCACTTTC 884
 QY 826 ATCTGGAAGATCTCAGACTTCCGCAAGAGCTCCAGGAAGCTGTGGCTGGCGGCAATCCC 885
 Db 885 CTGTGGAAGATCACCAGTGTTCACCAGGCGGTGCCATGATCGGCTGTGGCAGGACCGTC 944
 QY 886 GCATCTTCTCTCCAGCGCTTTACACACGAGGTACGGCTACCAAGATGTGTCTGGGTATC 945
 Db 945 AGCTCTTCTCTCCAGCGCTTTACACTGCCAAGTATGCTACAAAGTTGTGTCTGGGTG 1004
 QY 946 TACCTGAACGGGAGCGGACCGGGGAGAGAACACACTGTGTCCCTCTTCTTTGTGTGTATG 1005
 Db 1005 TACCTGATTGGAGATGGCACCTGGAAGAGAACCCATCTTTCGCTCTTCATCGTATCATG 1064
 QY 1006 AAGGGCCGAATGACGCGCTGTGCGGTGGCGCTTCAACCAAGAGGTGACCTTAAATGCTG 1065
 Db 1065 AGAGGGGAGTATGATGCGCTGTGCGGTGGCGCTTTCGGAACAAGTACCTTCAATGCTG 1124
 QY 1066 CTCGACCAAGATTAACGGGAGCACGTGATTGACGCTTTCAGGCGGAGCGTGAATTCATCC 1125
 Db 1125 CTGGACCAAGACACCGGTGAGCAGCGCATTTGAGCGCTTCCGCGCTGACCTAAGCTCAGCG 1184
 QY 1126 TCTTTTCAGAGGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCTCTTCTGCCCC 1185
 Db 1185 TCTTCCAGAGGCCCGGAGTGAACCAACGTGGCAGTGGATGCCACTCTTCTTCCCC 1244
 QY 1186 GTCTCCAAGATGGAGGCAAGAAATTCCTAC--GTGCGGAGCGATGCCATCTTTCATCAAG 1243
 Db 1245 CTCAGCAAACTGCAGTCAACCAAGCACCGCTAGTGAAGGACGACACAATGTTCTCAAGT 1304
 QY 1244 CCATTGTGGA 1253
 Db 1305 GCATTGTGGA 1314

RESULT 11
 US-09-417-540-7
 ; Sequence 7, Application US/09417540
 ; Patent No. 6639052
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
 ; APPLICANT: Jian Ni and Jing-Shan Hu
 ; TITLE OF INVENTION: Human Genes, Sequences and
 ; TITLE OF INVENTION: Expression Products
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/417,540
 ; FILING DATE: 14-Oct-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/705,771
 ; FILING DATE: August 30, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; REFERENCE/DOCKET NUMBER: 325800-346 (PFI96)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 973-994-1700

```

; TELERAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2361 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-417-540-7

Query Match      21.8%; Score 276.8; DB 4; Length 2361;
Best Local Similarity 64.3%; Pred. No. 3.7e-59;
Matches 431; Conservative 0; Mismatches 237; Indels 2; Gaps 1;

QY 586 CTGGAGAAAGACGGCCACTTTGAGACATTTGCTGCTCAACCGGAGGTGGAG 645
DB 645 CTGGAGGGAAGCTGCGTGTGTTGAGAACATGTTGCTCTCAACAGGAGGTGGAG 704
QY 646 AGGGTGGCCATGACTGCCGAGGCGCTGCAGCGGAGCACCGGCTGGACCAAGATT 705
DB 705 GCCTCCCACTGGCCCTGGCCACTCTATCCACGAGGCGAGCTGGACCGGCATC 764
QY 706 GAAGCCCTGAGTAGCAAGGTGAGCGAGCTGGAGAGGAGCATTTGGCTCAAGACCTGGG 765
DB 765 CTGAGCTTGGAGCAGAGGCTGTGTCAGGTTTCAGCAGACCCCTGCCAGAAACAGGCG 824
QY 766 ATGCTGACTTGGAGCAGAGGCTTTGGAGATGGAGGCATCCACCTACGATGGGTCTTC 825
DB 825 CTGGCAAGCTGGAGCAGAGCTTGGCCCTCATGGAGGAGCCCTCTTCATGGCACTTC 884
QY 826 ATCTGGAAGATCTCAGACTTGGCCAGAGAGCTTCCAGGAAGCTGTGGCTGGCGCATACC 885
DB 885 CTGTGGAAGATCAACAGTGTCAACAGCGGCTGTCATGAGTCGGCCCTGTGGCAGGAC 944
QY 886 GCATCTTCTCCCGCCCTTCTACACGAGGATGAGCTAGAGATGTTGCTGCTATC 945
DB 945 AGCCTCTTCTCCCGCCCTTCTACATGCAAGTATGGCTACAGTTGCTGCTGGCTG 1004
QY 946 TACTTGAACGGCGACGGCCGCGGAGGAACACACCTGTTCCTTTGTTGTTGATG 1005
DB 1005 TACTTGAATGGAGATGGCACTGGAAGAGAACCCATCTTTGCTCTTCATCGTATCATG 1064
QY 1006 AAGGGCCGATACGCGCTGCTGCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG 1065
DB 1065 AGAGGGGAGTATGATGCGCTGCTGCGGTGGCCCTTCCGGAACAGGTACCTTCATGCTG 1124
QY 1066 CTGACAGAAATAACGGGAGCAGCTGATGAGCCCTTCAGGCGCCGACGTGACTTCATCC 1125
DB 1125 CTGACAGAAACAACTGTGAGCAGCGCATTTGACGCTTCGGGCTGACCTAAGCTCAGCG 1184
QY 1126 TCTTTTCAGAGGCGAGTCAACGACATGAACATCGAAGGCTGCGCCCTCTCTGCCCC 1185
DB 1185 TCTTTCAGAGGCGGAGAGTGAACCAACGTCGCGGAGTGGATGCGCCACTCTTTCTCCCC 1244
QY 1186 GTCTCCAGATGGAGGCAAGAAATTCCTAC - GTGCGGAGCATGCGATCTTCATCAAG 1243
DB 1245 CTAGCAAACTGAGTACCCAGACGCGCTAGTAAGGACGACAAATGTTCTCTCAAGT 1304
QY 1244 CCATTGTGGA 1253
DB 1305 GCATTGTGGA 1314

RESULT 12
US-08-331-394-1
; Sequence 1, Application US/08331394
; Patent No. 5670319
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor
; RECEPTOR-ASSOCIATED FACTORS

```

```

; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,394
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3215
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-331-394-1

Query Match      21.4%; Score 272; DB 1; Length 2088;
Best Local Similarity 63.8%; Pred. No. 5.5e-58;
Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 586 CTGAGAAAGAGAGCGGCACCTTTTGAGAACATTTCTGCGCTCTGAACCGGAGGTGGAG 645
DB 773 CTGGAGGAGAGAGCTGCGTGTGTTTGAACATTTGCTGCTCTCAACAGGAAGTGGAG 832
QY 646 AGGGTGGCCATGACTGCCGAGGCGCTGCAGCGGAGCACCGGCTGGACCAAGATT 705
DB 833 GCTTCCCACTTGGCACTGGCCGCTCATCCACGAGGCGAGTTGGACCGAGACCTC 892
QY 706 GAAGCCCTGAGTAGCAAGGTGCAGCGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCG 765
DB 893 CTGAGCTTGGAGCAGAGGCTGTGGAATTAACAGCAAAACCTGGCTCAAAAAGACAGGTC 952
QY 766 ATGCTGACTTGGAGCAGAAAGTCTTGGAGATGGAGGATCCACCTAGATGGGTCTTC 825
DB 953 CTGGCAAGCTTGAGCAGCTGCGACTATGGAGAGGAGCATCTTTGATGGTACTTTC 1012
QY 826 ATCTGGAAGATCTCAGACTTCCGAGGAAGTCCAGGAAGCTGTGGCTGGCGCATACC 885
DB 1013 CTGTGGAAGATCAACCAATGTACCAAGCGGTGCCAGAGTCAGTGTGTGGCGGACTGC 1072
QY 886 GCCATCTTCTCCCGCCCTTCTACACGAGAGGTACGCTACAGATGTGTCTGGTATC 945
DB 1073 AGCCTCTTCTCTCCAGCTTTCTACACTGCCAAGTATGGTTTCAAGTTGTGGCTGGCTTG 1132
QY 946 TACCTGAACGGGCGGCGACCGGCGGAGGAACACACCTGTGCCCTCTCTTTGTGGTATG 1005
DB 1133 TACCTGAACGGGAGTGGCTCAGGCAAGAGAGACCCACCTGTCCCTCTCATGATCATG 1192
QY 1006 AAGGGCCGGAATGACGCGCTGCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG 1065
DB 1193 AGAGGAGAATACGATGCTCTCTGCGCTTTCAGGAAACAGGTCACTTTATGCTA 1252
QY 1066 CTCGACCAAGAAATACCGGGAGGACCGATGATGAGCGCTTCAGGCCGAGCGTGAATTCATCC 1125

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Db 1253 CTGACCAAGAACCGAGAGCATGCTATGTAGCTTCCGGCTGACCTGAGCTCAGCC 1312
 QY 1126 TCTTTTCAGAGCCAGTCAACACATGAACTCGCAAGCGGCTGCCCTCTTCTGCCCC 1185
 Db 1313 TCTTCCAGCGCCACAGAGTGAGACCAAGTGCGGCGGCTGCCCTCTTCTTCCCC 1372
 QY 1186 GTCTCCAGATGAGGCA---AAGAAATTCCTACGTGCGGCGGAGTGCATCTTCATCAAG 1242
 Db 1373 CTCAGAGCTGCACTGACCCCAAGCAAGCTACGTCAAAGATGACACAATGTCTCTCAA 1432
 QY 1243 GCCATTGTGGAC 1254
 Db 1433 TGCATTGTGGAC 1444

RESULT 13

US-08-250-858-1
 ; Sequence 1, Application US/08250858
 ; Patent No. 5708142
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; APPLICANT: Rothe, Mike
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 62
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/250,858
 ; FILING DATE: 27-May-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,065
 ; REFERENCE/DOCKET NUMBER: 897.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3216
 ; TELEFAX: 415/952-9891
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2088 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-250-858-1

Query Match 21.4%; Score 272; DB 1; Length 2088;
 Best Local Similarity 63.8%; Pred. No. 5.5e-58;

Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 586 CTGAGAGAGAGCGGCCACTTTTGAGAACATTTGCTGCGTCTGAACCGGAGGTGGAG 645
 Db 773 CTGAGAGAGAGCTGCGTGTGTTGCAACATTTGCTGCTCAACAGGAAGTGGAG 832
 QY 646 AGGCTGCCATGACTCGGAGGCTCGACCGGACGAGCTGACCAACAGCAAGATT 705
 Db 833 GCTTCCCACTGGCACTGGCGCGCTCCATCCACGAGCGAGTTGACCGAGCACCTC 892
 QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGGAGGAGGAGCATTTGGCTCAAGGACCTGGCG 765

Db 893 CTGAGCTTGAGCAGAGGCTGGTGAATTTACAGCAAAACCTGGCTCAAAAACAGCAGGTC 952
 QY 766 ATGCTGACTTGGAGCAGAGGCTTGGAGATGGAGGATCCACCTACGATGGGTCTTC 825
 Db 953 CTGGGCAAGCTTGAGCACAGTCTGCGACTCATGGAGGAGGCATCCTTTGATGGTACTTTC 1012
 QY 826 ATCTGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCCGCATACCC 885
 Db 1013 CTGTGAAGATCACCAATGTCAACCAAGCGGTGCCAGAGTCAAGTGTGGCCGAGTGTTC 1072
 QY 886 GCATCTTCTCCAGCCTTCTACACCAAGAGTACGGCTCAAGATGTTCTGGTATTC 945
 Db 1073 AGCCTCTTCTCCAGCTTCTACACTGCCAAATATGGTTACAAAGTTGTGCTGGCTTG 1132
 QY 946 TACCTGAACGGGACGGCACCGGCGGAGGAACACACCTGTGCTCTTCTTGTGGTGTG 1005
 Db 1133 TACCTGAACGGGATGGCTCAGGCAAGAGACCCACCTGTCTCTTCTCATGTGATCATG 1192
 QY 1006 AAGGCCCCGAATGACGCCCTGTGCGGTGGCCCTTCAACCAAGAGTGAACCTTAATGCTG 1065
 Db 1193 AGAGGAGAATACGATGCTCTCTGCTGCCCTTTCAGGAACAAGTCACTTTATGCTA 1252
 QY 1066 CTCGACCAGAAATACCGGAGACAGTGTGACGCTTTCAGGCGGAGTGAACCTTCATCC 1125
 Db 1253 CTGACCAGAACACCGAGAGATGCTATTGATGCTTCCGCGCTGACCTGAGCTCAGCC 1312
 QY 1126 TCTTTTCAGAGCCAGTCAACGACATGAACATGCAAGCGGTGCCCTCTTCTTGCCTCC 1185
 Db 1313 TCTTCCAGCGCCACAGAGTGAGACCAAGTGGCCAGCGCTGCCCTCTTCTTCTCC 1372
 QY 1186 GTCTCCAGATGAGGCA---AAGAAATTCCTACGTGCGGAGCATGCCATCTTCATCAAG 1242
 Db 1373 CTCAGAGCTGCACTGACCCCAAGCAAGCTACGTCAAAGATGACACAATGTCTCTCAA 1432
 QY 1243 GCCATTGTGGAC 1254
 Db 1433 TGCATTGTGGAC 1444

RESULT 14

US-08-446-915-1
 ; Sequence 1, Application US/08446915
 ; Patent No. 5741667
 ; GENERAL INFORMATION:
 ; APPLICANT: Goedel, David V.
 ; APPLICANT: Rothe, Mike
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,915
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/250858
 ; FILING DATE: 27-May-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/331394
 ; FILING DATE: 28-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-446-915-1

Query Match 21.4%; Score 272; DB 1; Length 2088;
Best Local Similarity 63.8%; Pred. No. 5.5e-58;
Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 586 CTGGAGAGAGAGCGGCCACTTTTGAGAACATTGTCGCTGCTGAAACCGGAGGTGGAG 645
DB 773 CTGGAGAGAGAGCGGTGTTGCAACATTGTTGCTCTCAACAGGAAGTGGAG 832
QY 646 AGGTGGCCATGATCGCGAGGCTGAGCGGAGCAGCCGGCTGGACCAAGACAAATT 705
DB 833 GCTTCCACCTGGCACTGGCGGCTCCATCCAGAGAGCCAGTTGGACCGAGACCTC 892
QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGGAGAGAGCATTTGGCTCAAGGACCTGGCG 765
DB 893 CTGAGCTTGGAGCAGAGGTTGGTGAATTACAGCAACCTGGCTCAAAAGACCGATC 952
QY 766 ATGCTGATTTGGAGAGAAAGTCTTGGAGATGAGGCAATCCACTAGATGGGTCTTC 825
DB 953 CTGGCAAGCTTGAGACAGCTGCGACTCATGAGGAGGATCTCTTGTGATGTTACTTTC 1012
QY 826 ATCTGGAGAGTCTCAGATTCGCCAGGAAGCTCCAGGAAGCTGGTGGCGGCATACCC 885
DB 1013 CTGTGGAAGATACCAATGTACCAGCGGTGCCAGCAGTCAGTGTGTGGCGGACTGTC 1072
QY 886 GCCATCTTCTCCAGCCCTTCTACACAGCAGGATGAGGCTACAGATGTGTGCGGTATC 945
DB 1073 AGCCTCTTCTCCAGCTTCTACACTGCCAAGTATGTTACAAAGTGTGTGCTGCGTTG 1132
QY 946 TACCTGAACGGGACCGGCACCGGCGGAGGACACACCTGCTCTCTTCTTTGTGGTATG 1005
DB 1133 TACCTGAACGGGATGGCTCAGGCAAGAACCCACCTGTCTCTTCTTATCGTATCATG 1192
QY 1006 AAGGCGCCGAATGACGCGCTCTGCGGTGGCCCTTCAACCAAGAGGTGACCTTAATGTC 1065
DB 1193 AGAGGAGATACGATGCTCTCTGCGCTGGCTTTCAGGAACAAAGGTCACTTTATGCTA 1252
QY 1066 CTGACCAAGATTAACCGGAGCAGTGTGACGCTTCAGGCGGAGCTGACTTCATCC 1125
DB 1253 CTTGACCAAGAACACCGAGAGCATGTTATGATGCTTCGGCTGACCTGAGCTCAGCC 1312
QY 1126 TCTTTTTCAGAGGCGAGTCAACGACATGAACATGCAAGGGGTGCGCCCTCTTCTGCCCC 1185
DB 1313 TCCTTCAGGCGGCACAGAGTGAGACCAAGGTGGCCAGCGGTGCGCGCTCTTCTTCCCC 1372
QY 1186 GTCTCCAGATGAGGCA---AGAAATCTCTAGTGGGAGCATGCCATCTTCATCAAG 1242
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DB 1433 TGCATTGTGGAC 1444

RESULT 15
US-08-744-139-1
; Sequence 1, Application US/08744139
; Patent No. 5869612
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V

APPLICANT: Rothe, Mike
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,139
FILING DATE: 31-Oct-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/250858
FILING DATE: 05/27/1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-744-139-1

Query Match 21.4%; Score 272; DB 2; Length 2088;
Best Local Similarity 63.8%; Pred. No. 5.5e-58;
Matches 429; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 586 CTGGAGAGAGAGCGGCCACTTTTGAGAACATTGTCGCTGCTGAAACCGGAGGTGGAG 645
DB 773 CTGGAGAGAGAGCTGCGTGTGTTGCAACATTGTTGCTCTCAACAGGAAGTGGAG 832
QY 646 AGGTGGCCATGATCGCGAGGCTGAGCGGAGCAGCCGGCTGGACCAAGACAAATT 705
DB 833 GCTTCCACCTGGCACTGGCGGCTCCATCCAGAGAGCCAGTTGGACCGAGACCTC 892
QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGGAGAGAGCATTTGGCTCAAGGACCTGGCG 765
DB 893 CTGAGCTTGGAGCAGAGGTTGGTGAATTACAGCAACCTGGCTCAAAAGACCGATC 952
QY 766 ATGCTGATTTGGAGAGAAAGTCTTGGAGATGAGGCAATCCACTAGATGGGTCTTC 825
DB 953 CTGGCAAGCTTGAGACAGCTGCGACTCATGAGGAGGATCTCTTGTGATGTTACTTTC 1012
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QY 886 GCCATCTTCTCCAGCCCTTCTACACAGCAGGATGAGGCTACAGATGTGTGCGGTATC 945
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Qy	1066	CTCGACCAAGATACCGGAGACCGTGAATTGACGCTTTCAGGCCGACGTCATTC	1125
Db	1253	CTTGACCAAGACACCGAGAGCATGCTATTGATGCTTCCGGCCTGACCTGAGCTCAGCC	1312
Qy	1126	TCTTTTTCAGAGCCAGTCAACGACATGAACATCGCARGCGGCTGCCCTCTTCTGCCCC	1185
Db	1313	TCCTTCCAGCGGCCACAGAGTGAGACCAACGTGGCCAGCGGCTGCCCTCTTCTTCCCC	1372
Qy	1186	GTCTCCAGATGGAGCA---AAGAAATTCCTACGTGGCGGACGATGCCATCTTCATCAAG	1242
Db	1373	CTCAGCAAGCTGCAGTCACCCAAAGCAGCGCTACGTCAAGATGACACAATGTTCTCTCAA	1432
Qy	1243	GCCATTGTGGAC	1254
Db	1433	TGCATTGTGGAC	1444

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 20:48:57 ; Search time 701 Seconds

(without alignments)
9746.709 Million cell updates/sec

Title: US-10-018-030B-1

Perfect score: 1269

Sequence: 1 atgggtcgagctagctgac.....tggacctgacagggctctaa 1269

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
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- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959.6	75.6	1506	US-10-361-270-2	Sequence 2, Appli
2	959.6	75.6	2262	US-09-962-832-121	Sequence 121, Appl
3	959.6	75.6	2262	US-09-954-456-1186	Sequence 1186, Ap
4	959.6	75.6	2262	US-10-067-125-2	Sequence 2, Appli
5	855.6	67.4	2094	US-10-094-749-63	Sequence 63, Appl
6	701	55.2	2121	US-10-283-500-3	Sequence 3, Appli
7	286.6	23.4	1251	US-10-085-117-330	Sequence 330, App
8	286.6	23.4	2380	US-10-067-125-1	Sequence 1, Appli
9	286.6	23.4	2380	US-10-172-118-1184	Sequence 1184, Ap
10	286.6	23.4	2380	US-10-085-117-329	Sequence 329, App
11	286.6	23.4	2380	US-10-342-887-1184	Sequence 1184, Ap
12	286.6	23.4	5981	US-10-044-090-823	Sequence 823, App

13	276.8	21.8	2361	US-10-453-478-7	Sequence 7, Appli
14	272	21.4	481	US-09-918-995-28886	Sequence 28886, A
15	272	21.4	1230	US-10-085-117-327	Sequence 327, Appl
16	272	21.4	2088	US-10-283-500-1	Sequence 1, Appli
17	272	21.4	2088	US-10-085-117-326	Sequence 326, App
18	190.8	15.0	354	US-09-796-692-5702	Sequence 5702, Ap
19	190.8	15.0	354	US-10-040-862-5702	Sequence 5702, Ap
20	190.8	15.0	354	US-10-057-475B-5702	Sequence 5702, Ap
21	190.8	15.0	354	US-10-154-884B-5702	Sequence 5702, Ap
22	190.8	15.0	354	US-10-764-324-5702	Sequence 5702, Ap
23	189.2	14.9	354	US-09-796-692-5613	Sequence 5613, Ap
24	189.2	14.9	354	US-10-040-862-5613	Sequence 5613, Ap
25	189.2	14.9	354	US-10-057-475B-5613	Sequence 5613, Ap
26	189.2	14.9	354	US-10-154-884B-5613	Sequence 5613, Ap
27	189.2	14.9	354	US-10-764-324-5613	Sequence 5613, Ap
28	171.6	13.5	1581	US-10-262-445-129	Sequence 129, App
29	171.6	13.5	1661	US-10-042-865-49	Sequence 49, Appl
30	171.6	13.5	1707	US-10-262-445-131	Sequence 131, Appl
31	171.6	13.5	1787	US-10-042-865-37	Sequence 37, Appl
32	171.6	13.5	2738	US-09-968-007A-803	Sequence 803, App
33	171.6	13.5	3480	US-10-004-378A-3	Sequence 3, Appli
34	171.6	13.5	3675	US-10-004-378A-1	Sequence 1, Appli
35	171.6	13.5	3993	US-10-067-125-5	Sequence 5, Appli
36	171.6	13.5	3993	US-10-172-118-2	Sequence 2, Appli
37	171.6	13.5	3993	US-10-342-887-2	Sequence 2, Appli
38	151.8	12.0	2359	US-08-813-323A-3	Sequence 3, Appli
39	146.6	11.6	1792	US-09-950-302-3	Sequence 3, Appli
40	146.6	11.6	2240	US-10-242-212-6	Sequence 6, Appli
41	146.6	11.6	2339	US-10-207-655-102	Sequence 102, App
42	146.6	11.6	2065	US-09-950-902-1	Sequence 1, Appli
43	145	11.4	2455	US-08-813-323A-4	Sequence 4, Appli
44	145	11.4	2455	US-10-067-125-3	Sequence 3, Appli
45	145	11.4	2455	US-10-067-125-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-361-270-2
; Sequence 2, Application US/10361270
; Publication No. US20040038299A1
; GENERAL INFORMATION:
; APPLICANT: Kuai, Jun
; APPLICANT: Wooters, Joseph L
; APPLICANT: Nickbarg, Elliott
; APPLICANT: Qiu, Yongchang
; APPLICANT: Lin, Lin-Ling
; TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
; FILE REFERENCE: 22058-565
; CURRENT APPLICATION NUMBER: US/10/361,270
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/355,183
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-361-270-2

Query Match 75.6%; Score 959.6; DB 16; Length 1506;
Best Local Similarity 81.7%; Pred. No. 7.5e-271;
Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

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DB	1	ATGGCTGACGTAGCTGACCCCTGGCTCCCTGGAGTTGCTACACCGCGGCTTCTCC	60
QY	61	AAAGCCCTCTGGGACCAAGCTGGAAGCAAGTGTGTGCTCGCTGCAGAACGTC	120

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 Qy 121 CTCGACGACCCCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTCTGCTGCTGGCCAGC 180
 Db 121 CTCGACGACCCCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTCTGCTGCTGGCCAGC 180
 Qy 181 ATCCTCAGCTCTGGGCTTCAGAACTGTGCTGCTGTGTTCAAGAGGCGATATATGAAGAA 240
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 Qy 301 GAGAGCTTCGCGCCGCTGTGCTCCAGTATGATGATGACCTCGAAGAGGAGACCTCGAAGAA 360
 Db 301 GAGAGCTTCGCGCCGCTGTGCTCCAGTATGATGATGACCTCGAAGAGGAGACCTCGAAGAA 360
 Qy 361 TACG----- 364
 Db 361 TACGAGAGCTGCCACGAAGGGCGCTGCCCGCTCATGTGACCGAATGTCCGCGGTGAAA 420
 Qy 365----- 364
 Db 421 GGCCTGGTCCGCTTGGTGAAGAGGCGCCACCTGGAGCAGAGTCCCGGAGAGAAGC 480
 Qy 365----- 364
 Db 541 GTCTGCCCAAGTTCCTTAACTTGTGACGGCTGCGGCAAGAGAGATCCCCCGGGAG 600
 Qy 365 -AGTTTCAGACACAGTCAAGACTTGTGGGAAGTGTGAGTCCCTTCGATTCAGATCCAGCC 423
 Db 601 AAGTTTCAGACACAGTCAAGACTTGTGGGAAGTGTGAGTCCCTTCGATTCAGATTCACGCC 660
 Qy 424 ATCGCTCCCTCGAGACGCTAGGGTGTAGAAACAGCAGGAGCAGAGGTGCGATGGCTG 483
 Db 661 ATCGCTCCCTCGAGACGCTAGGGTGTAGAAACAGCAGGAGCAGAGGTGCGATGGCTG 720
 Qy 484 CGGAGACCTCGGCACTACTAGTTCGCTGCTGAGGCAAGCCCTCTTTGGAGAC 543
 Db 721 CGGAGACCTCGGCACTACTAGTTCGCTGCTGAGGCAAGCCCTCTTTGGAGAC 780
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 Qy 604 ACTTTTGAAGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 663
 Db 841 ACTTTTGAAGAACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 Qy 664 GAGGCTTCAGCCGCGAGCAGCAGCTGGAACAGACAAAGATTGAGCCCTGAGTACGAAG 723
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 Qy 724 GTGACAGCAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTTGGAGCAG 783
 Db 961 GTGACAGCAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTTGGAGCAG 1020
 Qy 784 AAGTCTTGGAGATGGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTTGGAGATCT 843
 Db 1021 AAGTCTTGGAGATGGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTTGGAGATCT 1080
 Qy 844 TTCCGACGAGGAGCTTCAGGAGAGCTGTGGCTGGCGGATACCCGCGATCTTCTCCCGAGCC 903
 Db 1081 ATCTTCAAGGAGCTTCAGGAGAGCTGTGGCTGGCGGATACCCGCGATCTTCTCCCGAGCC 1140
 Qy 904 TTCTTACACGAGGATGAGGAGCTTCAAGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
 Db 1141 TTCTTACACGAGGATGAGGAGCTTCAAGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200

RESULT 2

US-09-962-832-121
 ; Sequence 121, Application US/09962832
 ; Patent No. US20020110821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ebner, Reinhard
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur
 ; FILE OF INVENTION: Sets
 ; FILE REFERENCE: 689290-74
 ; CURRENT APPLICATION NUMBER: US/09/962,832
 ; CURRENT FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,077
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,280
 ; PRIOR FILING DATE: 2000-09-25
 ; NUMBER OF SEQ ID NOS: 259
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 121
 ; LENGTH: 2262
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-962-832-121

Query Match 75.6%; Score 959.6; DB 9; Length 2262;
 Best Local Similarity 81.7%; Pred. No. 8.4e-271;
 Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;

Qy 1 ATGGCTGACGTAGCGTGACCCCGCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 60
 Db 55 ATGGCTGACGTAGCGTGACCCCGCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 114
 Qy 61 AAGACCCCTCTCGGGACCAAGCTGGAAGCCCAAGTACCTGCTCCGCTGCAGAAACGTC 120
 Db 115 AAGACCCCTCTCGGGACCAAGCTGGAAGCCCAAGTACCTGCTCCGCTGCAGAAACGTC 174
 Qy 121 CTCGACGACCCCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTCTGCTGCTGGCCAGC 180
 Db 175 CTCGACGACCCCTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTCTGCTGCTGGCCAGC 234
 Qy 181 ATCCTCAGCTCTGGGCTTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 235 ATCCTCAGCTCTGGGCTTCAGAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 294
 Qy 241 GGCATTTCTATTTTAAAGACAGTTCGGCCCTTCCAGATATGCTGCGCCGAGGAGGTG 300
 Db 295 GGCATTTCTATTTTAAAGACAGTTCGGCCCTTCCAGATATGCTGCGCCGAGGAGGTG 354

QY 301 GAGAGCTGCGGCGCTGTGTCCAGTGATGACCTGGAAGGGGACCTGTAAGAA 360
Db 355 GAGAGCTGCGGCGCTGTGTCCAGTGATGACCTGGAAGGGGACCTGTAAGAA 414
QY 361 TAGG----- 364
Db 415 TACGAGAGTGCACGAGGCGCTGCCCGCTCATGCTGACCGAATGTCCCAGTGTAA 474
QY 365----- 364
Db 475 GGCCTGGTCGCTTGGTGAAGAGGCGCCACCTGGAGCAGAGTGCCCGAGAGAAGC 534
QY 365----- 364
Db 535 CTGAGCTGCGGCGATTCGCGGCGACCTGTCTGGAGCAGACGTGAAGCGCACACAGAG 594
QY 365----- 364
Db 595 GTCGCCCCAAGTCCCTTAATCTGTGACGGCTGGCGCAAGAAATCCCCCGGAG 654
QY 365 -AGTTTCAGGACCACTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCCACGCC 423
Db 655 AAGTTTCAGGACCACTCAAGACTTGTGGCAAGTGTGAGTCCCTTGCAGATTCCACGCC 714
QY 424 ATCGCTGCTCGAGACGCTAGAGGTGAGAAACAGCAGAGCAGACAGAGTGCAGTGGCTG 483
Db 715 ATCGCTGCTCGAGACGCTAGAGGTGAGAAACAGCAGAGCAGACAGAGTGCAGTGGCTG 774
QY 484 CGGAGCAGCTGCGCCTGCTACTGAGCTGGAGGCAAGCCCTCTGGAGAGAC 543
Db 775 CGGAGCAGCTGCGCCTGCTACTGAGCTGGAGGCAAGCCCTCTGGAGAGAC 834
QY 544 CAGAGCCAGCGGGGTGAGAGTCTTCAGAGGTGCGAGAGCTGCGAGAAAGACGGCC 603
Db 835 CAGAGCCAGCGGGGTGAGAGTCTTCAGAGGTGCGAGAGCTGCGAGAAAGACGGCC 894
QY 604 ACTTTTGAAGAACTTCTGCGTCCCTGAACCGGAGGTGAGAGGTGCCATGACTGCC 663
Db 895 ACTTTTGAAGAACTTCTGCGTCCCTGAACCGGAGGTGAGAGGTGCCATGACTGCC 954
QY 664 GAGGCTTGACCGCGGAGCAGCAGCTGGACCAAGAAAGATTGAAGCCCTGAGTAGCAAG 723
Db 955 GAGGCTTGACCGCGGAGCAGCAGCTGGACCAAGAAAGATTGAAGCCCTGAGTAGCAAG 1014
QY 724 GTCAGCAGCTGAGAGAGCAGTGGCTCAAGGACCTGCGATGCTGACTGAGAGCAG 783
Db 1015 GTCAGCAGCTGAGAGAGCAGTGGCTCAAGGACCTGCGATGCTGACTGAGAGCAG 1074
QY 784 AAGGTCTTGAGATGAGGAGCATCCACTACATGGGGTCTTCACTGGAAGATCTCAGAC 843
Db 1075 AAGGTCTTGAGATGAGGAGCATCCACTACATGGGGTCTTCACTGGAAGATCTCAGAC 1134
QY 844 TTCGCCAGGAAGTCCAGGAAGCTGTGGTGGCGGATACCGCCATCTTCTCCCGAGCC 903
Db 1135 ATCTCAGGAAGTCCAGGAAGCTGTGGTGGCGGATACCGCCATCTTCTCCCGAGCC 1194
QY 904 TTCTACACGAGGATGAGCTACAGATGCTGCTGGTATCTACCTGAACGCGCAGCGC 963
Db 1195 TTCTACACGAGGATGAGCTACAGATGCTGCTGGTATCTACCTGAACGCGCAGCGC 1254
QY 964 ACCGGGCGAGGAACACACCTGTCCCTCTTTTGTGGTGAAGGCGCCGGAATGACGCC 1023
Db 1255 ACCGGGCGAGGAACACACCTGTCCCTCTTTTGTGGTGAAGGCGCCGGAATGACGCC 1314
QY 1024 CTGCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACAGGATACCGG 1083
Db 1315 CTGCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACAGGATACCGG 1374
QY 1084 GAGCAGCTGATTGAGCGCTTCAGGCCCGAGCTGACCTTCATCTCTTTTTCAGAGGCCAGTC 1143
Db 1375 GAGCAGCTGATTGAGCGCTTCAGGCCCGAGCTGACCTTCATCTCTTTTTCAGAGGCCAGTC 1434
QY 1144 ACGCATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCCTCTTCCAAAGATGGAGGA 1203

Db 1435 AACGACATGAACATCGCAAGCGGTGCCCTCTTCTGCCCCGTCTCCAAGATGGAGGA 1494
QY 1204 AAGAAATTCCTACGTCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTTGACAGGG 1263
Db 1495 AAGAAATTCCTACGTCGGGACGATGCCATCTTCATCAAGGCCATTGTGGACCTTGACAGGG 1554
QY 1264 CTCTAA 1269
Db 1555 CTCTAA 1560
RESULT 3
US-09-954-456-1186
; Sequence 1186, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1186
Query Match 75.6%; Score 959.6; DB 9; Length 2262;
Best Local Similarity 81.7%; Pred. No. 8.4e-271; Indels 237; Gaps 1;
Matches 1230; Conservative 0; Mismatches 39;
QY 1 ATGGCTGAGCTAGCGTGACCCCTCGCTGAGTTGCTTACAGCCCGGTTCTCC 60
Db 55 ATGGCTGAGCTAGCGTGACCCCTCGCTGAGTTGCTTACAGCCCGGTTCTCC 114
QY 61 AAGACCTCTCTGGGACCAAGCTGGAAGCAGTACCTGCTGCTCGGCTGCAGAAAGTC 120
Db 115 AAGACCTCTCTGGGACCAAGCTGGAAGCAGTACCTGCTGCTCGGCTGCAGAAAGTC 174
QY 121 CTCGCGAGCCCTTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTTCTGCTGGCCAGC 180
Db 175 CTCGCGAGCCCTTTCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTTCTGCTGGCCAGC 234
QY 181 ATCTCAGCTCTGGGCTCAGAACTGCTGCTGCTGCTTTCAGAGGGCATATATGAAGAA 240
Db 235 ATCTCAGCTCTGGGCTCAGAACTGCTGCTGCTGCTTTCAGAGGGCATATATGAAGAA 294
QY 241 GGCATTCTTATTTAGAAAGCAGTTTCGCGCTTCCAGATAATGTCGCCCGCAGGAGGTG 300

Db 295 GCAATTTCTATTTTAAAGACGATTCGGCTTCCAGATATGCTGCCCGCAGGAGGTG 354
 QY 301 GAGACCTGCGCGCGTCTGTCCAGTATGATGATGACCTCGAAGGGGACCTTGAAGAA 360
 Db 355 GAGAGCTGCGCGCGTCTGTCCAGTATGATGATGACCTCGAAGGGGACCTTGAAGAA 414
 QY 361 TAGC----- 364
 Db 415 TAGGAGAGTGCACGAAGGCGGTGCGCGTCACTGATGATGATGATGATGATGATGATG 474
 QY 365 ----- 364
 Db 475 GGCCTGCTCGCGTGTGTAAGAGGAGCGCACCTGGAGACGAGTGCCTGGAGAGAGC 534
 QY 365 ----- 364
 Db 535 CTGAGCTGCGCGCATTCGCGGACCTTGTCTCGGAGCAGACGTGAAGGCGCACCGAG 594
 QY 365 ----- 364
 Db 595 GTCTGCCCAAGTTCCCTTAACCTGTGACGGCTGCGCAAGAGAGATCCCCCGGAG 654
 QY 365 -AGTTTCAAGACCGTCAAGCTTGTGGCAAGTGTGAGTCCCTTGAAGTCCACGCC 423
 Db 655 AAGTTTCAAGACCGTCAAGCTTGTGGCAAGTGTGAGTCCCTTGAAGTCCACGCC 714
 QY 424 ATCGGCTGCTCGAGACGATGAGGTGAGAAACAGCAGGAGCAGAGTGCATGGCTG 483
 Db 715 ATCGGCTGCTCGAGACGATGAGGTGAGAAACAGCAGGAGCAGAGTGCATGGCTG 774
 QY 484 CGGAGACCTGCGCATCTACTGAGTCTGCTGAGGCAAGCCCTCTTGGAGAC 543
 Db 775 CGGAGACCTGCGCATCTACTGAGTCTGCTGAGGCAAGCCCTCTTGGAGAC 834
 QY 544 CAGAGCAGCGGGGTGAGACTCTCTGAGAGTGCAGAGCTGAGAGAGAGAGAGCGCC 603
 Db 835 CAGAGCAGCGGGGTGAGACTCTCTGAGAGTGCAGAGCTGAGAGAGAGAGAGCGCC 894
 QY 604 ACTTTTGAGAACATTTGCTGCTGCTGAAACCGGAGGTGAGAGGTGGCCATGACTGCC 663
 Db 895 ACTTTTGAGAACATTTGCTGCTGCTGAAACCGGAGGTGAGAGGTGGCCATGACTGCC 954
 QY 664 GAGCCTGACCGCGCAGCAGCTGGAACAGACAAAGATGAGAGCTGAGTAGCAAG 723
 Db 955 GAGCCTGACCGCGCAGCAGCTGGAACAGACAAAGATGAGAGCTGAGTAGCAAG 1014
 QY 724 GTGAGAGCTGAGAGAGGAGATTTGGCTCAAGACCTGCGGATGGCTGAGTAGCAG 783
 Db 1015 GTGAGAGCTGAGAGAGGAGATTTGGCTCAAGACCTGCGGATGGCTGAGTAGCAG 1074
 QY 784 AAGTCTTGGAGATGAGAGGATTCACCTAGAGGGGTCTTCACTGGAAGATCTCAGAC 843
 Db 1075 AAGTCTGAGGCGCTTCCAGGCGCAGTGTGGCCACCGGTACTGCTCTCTGCTGGCCAGC 1134
 QY 844 TTCGCCAGGAGCTCCAGGAGCTGCTGCGCGCATACCGCCATCTTCTCCCGAGCC 903
 Db 1135 ATCTCAGAGAGCTCCAGGAGCTGCTGCGCGCATACCGCCATCTTCTCCCGAGCC 1194
 QY 904 TTCTACACGAGCTGAGGATGCTGAGATGCTGCTGATCTACCTGAACGGCGAGCGG 963
 Db 1195 TTCTACACGAGCTGAGGATGCTGAGATGCTGCTGATCTACCTGAACGGCGAGCGG 1254
 QY 964 ACCGGCGAGAAACACCTGCTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1023
 Db 1255 ACCGGCGAGAAACACCTGCTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1314
 QY 1024 CTGCTGCGGTGGCGCTTCAACAGAGGATGCTTAAATGCTGTCTGATCGACCAAGTAACCGG 1083
 Db 1315 CTGCTGCGGTGGCGCTTCAACAGAGGATGCTTAAATGCTGTCTGATCGACCAAGTAACCGG 1374
 QY 1084 GAGCAGCTGATGAGCGCTTCAAGCAGCGAGCTGAGCTTCACTCTTTTTCAGAGCGCAGTC 1143
 Db 1375 GAGCAGCTGATGAGCGCTTCAAGCAGCGAGCTGAGCTTCACTCTTTTTCAGAGCGCAGTC 1434

RESULT 4

US-10-067-125-2
 ; Sequence 2, Application US/10067125
 ; Publication No. US20030055015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Cowser, Lex M.
 ; APPLICANT: Monia, Brett P.
 ; APPLICANT: Xu, Xiaoxing S.
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
 ; FILE REFERENCE: ISPH-0321
 ; CURRENT APPLICATION NUMBER: US/10/067,125
 ; CURRENT FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: 09/167,109
 ; PRIOR FILING DATE: 1998-10-06
 ; NUMBER OF SEQ ID NOS: 228
 ; SEQ ID NO 2
 ; LENGTH: 2262
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (55)..(1560)
 ; PUBLICATION INFORMATION:
 ; DATABASE ENTRY NUMBER: U12597 Genbank
 ; DATABASE ENTRY DATE: 1996-02-16.
 US-10-067-125-2

Query Match 75.6%; Score 959.6; DB 14; Length 2262;
 Best Local Similarity 81.7%; Pred. No. 8.4e-271;
 Matches 1230; Conservative 0; Mismatches 39; Indels 237; Gaps 1;
 QY 1 ATGGCTGAGCTAGCTGACACCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 60
 Db 55 ATGGCTGAGCTAGCTGACACCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 114
 QY 61 AAGACCCCTCTGGGAGCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGAGAAAGCTC 120
 Db 115 AAGACCCCTCTGGGAGCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGAGAAAGCTC 174
 QY 121 CTCGCGAGCCCTTCCAGCGAGTGGCCACCGGTACTGCTCTCTCTGCTGCGCCAGC 180
 Db 175 CTCGCGAGCCCTTCCAGCGAGTGGCCACCGGTACTGCTCTCTCTGCTGCGCCAGC 234
 QY 181 ATCTCTCAGCTCTGGGCTCTCAGAACTGTCTGCTGTGTTCACGAGGGCATATATGAAG 240
 Db 235 ATCTCTCAGCTCTGGGCTCTCAGAACTGTCTGCTGTGTTCACGAGGGCATATATGAAG 294
 QY 241 GGCATTTCTATTTAGAAAGCAGTTGGCCCTTCCAGATAATGCTGCCCGCAGGAGGTG 300
 Db 295 GGCATTTCTATTTAGAAAGCAGTTGGCCCTTCCAGATAATGCTGCCCGCAGGAGGTG 354
 QY 301 GAGAGCCCTGCGCGCGTCTGTCCAGATGATGATGATGATGATGATGATGATGATGATG 360
 Db 355 GAGAGCCCTGCGCGCGTCTGTCCAGATGATGATGATGATGATGATGATGATGATGATG 414
 QY 361 TAGC----- 364
 Db 415 TACGAGAGCTGCCACAGGCGCGCTGCCCGCTCATGTGTGACCGCAATGTCCCGCGTGTAA 474

QY 365 ----- 364
 Db 475 GGCCTGGTCCGCTTGGTGAAGAGAGCCACCTGGAGACGAGTGCCTGGAGAGAGC 534
 QY 365 ----- 364
 Db 535 CTGAGTGGCGGATTCGCGGACCCCTGCTGCGGAGCAGAGTGAAGGCGCACCAGAG 594
 QY 365 ----- 364
 Db 595 GTCTGCCCCAAGTTCCTTAACTTTGTACGGCTGCGGCAAGAAGATCCCCGGGAG 654
 QY 365 -AGTTTCAGACACAGTCAAGACTTGTGCAAGTGTGAGTCCCTTGCAGATTCACAGCC 423
 Db 655 AAGTTTCAGACACAGTCAAGACTTGTGCAAGTGTGAGTCCCTTGCAGATTCACAGCC 714
 QY 424 ATCGGCTGCTCGAGACGGTAGAGGTGAGAAACAGCAGGAGCAGAGTGCAGTGGGTG 483
 Db 715 ATCGGCTGCTCGAGACGGTAGAGGTGAGAAACAGCAGGAGCAGAGTGCAGTGGGTG 774
 QY 484 CCGGAGCAGTGGCCATGCTACTGAGCTGGTGTGAGGCAAGCCCTCTTGGAGAC 543
 Db 775 CCGGAGCAGTGGCCATGCTACTGAGCTGGTGTGAGGCAAGCCCTCTTGGAGAC 834
 QY 544 CAGAGCCAGCGGGGTGAGAGTCTCTGAGAGGTGCGAGAGCTGAGAGAGAGAGAGAGCC 603
 Db 835 CAGAGCCAGCGGGGTGAGAGTCTCTGAGAGGTGCGAGAGCTGAGAGAGAGAGAGAGCC 894
 QY 604 ACTTTTGAGAAATTTCTGCTGCTGAGAACCGGAGGTGAGAGGTGAGAGGTGAGAGGTG 663
 Db 895 ACTTTTGAGAAATTTCTGCTGCTGAGAACCGGAGGTGAGAGGTGAGAGGTGAGAGGTG 954
 QY 664 GAGGCTGAGCGGAGCAGCGGTGAGAACCGGAGGTGAGAGGTGAGAGGTGAGAGGTGAG 723
 Db 955 GAGGCTGAGCGGAGCAGCGGTGAGAACCGGAGGTGAGAGGTGAGAGGTGAGAGGTGAG 1014
 QY 724 GTGACAGCTGAGAGAGAGATTTGGCTTCAAGGACCTGGGATGCTGACTTGGAGAG 783
 Db 1015 GTGACAGCTGAGAGAGAGATTTGGCTTCAAGGACCTGGGATGCTGACTTGGAGAG 1074
 QY 784 AGGTCTTGAGATGAGAGATCCACCTACGATGGGCTTCTATCTGGAAGATCTCAGAC 843
 Db 1075 AGGTCTTGAGATGAGAGATCCACCTACGATGGGCTTCTATCTGGAAGATCTCAGAC 1134
 QY 844 TTCCGAGGAGATCCAGGAGGTGAGTGGCTGGCGCATACCGGCTATCTTCCCGAGCC 903
 Db 1135 ATCTCTAGGAGGTCCAGGAGGTGAGTGGCTGGCGCATACCGGCTATCTTCCCGAGCC 1194
 QY 904 TTCTACACAGAGGTACGCTCAAGATGTGTCTGCTATCTACCTGAACGGGAGAGCC 963
 Db 1195 TTCTACACAGAGGTACGCTCAAGATGTGTCTGCTATCTACCTGAACGGGAGAGCC 1254
 QY 964 ACCGGGAGGAGACACACCTGCTCTTCTTTGTTGTTGATGAAGGGCCGATGACGCC 1023
 Db 1255 ACCGGGAGGAGACACACCTGCTCTTCTTTGTTGTTGATGAAGGGCCGATGACGCC 1314
 QY 1024 CTGCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACAGAGATTAACCGG 1083
 Db 1315 CTGCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACAGAGATTAACCGG 1374
 QY 1084 GAGCAGGTGATGAGCCCTTCAAGGAGGTGACCTTCACTCTCTTTTTCAGAGGCGAGTC 1143
 Db 1375 GAGCAGGTGATGAGCCCTTCAAGGAGGTGACCTTCACTCTCTTTTTCAGAGGCGAGTC 1434
 QY 1144 AAGCAGATGAACATCGCAAGCGGTGCGCCCTCTTCTGCGCCGCTTCCAGATGAGAGCA 1203
 Db 1435 AAGCAGATGAACATCGCAAGCGGTGCGCCCTCTTCTGCGCCGCTTCCAGATGAGAGCA 1494
 QY 1204 AAGAAATCTACGTGGGAGAGTGCATCTTCAAGGCCATTTGAGCCTGAGCAGG 1263
 Db 1495 AAGAAATCTACGTGGGAGAGTGCATCTTCAAGGCCATTTGAGCCTGAGCAGG 1554

QY 1264 CTCTAA 1269
 Db 1555 CTCTAA 1560
 RESULT 5
 US-10-094-749-63
 ; Sequence 63, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION: TAKAO
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOMYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3381
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 63
 ; LENGTH: 2094
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-094-749-63
 Query Match 67.4%; Score 855.6; DB 15; Length 2094;
 Best Local Similarity 81.5%; Pred. No. 2.6e-240;
 Matches 1095; Conservative 0; Mismatches 174; Indels 75; Gaps 6;
 QY 1 ATGGCTGAGCTAGCTGACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 60
 Db 45 ATGGCTGAGCTAGCTGACCCCTGGCTCCCTGGAGTTGCTACAGCCGGCTTCTCC 104
 QY 61 AAGACCTCTCTGGGAGCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGCGAGAAAGCTC 120
 Db 105 AAGACCTCTCTGGGAGCAAGCTGGAAGCCAAAGTACCTGTCTCCGCTGCGAGAAAGCTC 164
 QY 121 CTCGCGAGCCCTTCCAGGCGCAGTGGCCACCGGCTGCTCTCTTCTGCTGCGCCAGC 180
 Db 165 CTCGCGAGCCCTTCCAGGCGCAGTGGCCACCGGCTGCTCTCTTCTGCTGCGCCAGC 224
 QY 181 ATCTCTAGCTCTGGGCTCAGAACTGTCTGCTGTGTTCACGAGGCGATATATGAAGAA 240
 Db 225 ATCTCTAGCTCTGGGCTCAGAACTGTCTGCTGTGTTCACGAGGCGATATATGAAGAA 284
 QY 241 GGCATTTCTATTATAGAAAGCAGTTCCGCTTCCAGATATGCTGCCCGCAGGAGGTG 300
 Db 285 GGCATTTCTATTATAGAAAGCAGTTCCGCTTCCAGATATGCTGCCCGCAGGAGGTG 344
 QY 301 GAGACCTCTCCGCGCGCTGTGTCCAGTGATGGATGCACCTGGAAGGGGACCTTGAAGAA 360
 Db 345 GAGACCTCTCCGCGCGCTGTGTCCAGTGATGGATGCACCTGGAAGGGGACCTTGAAGAA 404
 QY 361 TACGAGTTTCA-----GGACACGCTCAAGACTTGTGGCAAGTGTGAGTCCCTT 409

Db 468 GGCCTGGTCCGCTCAGCGAGGAGGAGCACCACACTGACGAGAAATGCCCAAAAGGAGC 527
 QY 366 ----- 365
 Db 528 CTGAGCTGCCAGCACTGAGAGCACCCTGTAGCCACGTGGACCTGGAGGTACACTATGAG 587
 QY 366 ----- 365
 Db 588 GTCTGCCCAAGTTTCCCTTAACCTGTGATGGCTGTGGCAAGAGAGATCCCTCGGAG 647
 QY 366 --GTTTCAGACCACTCAAGACTTGTGGCAAGTGTGAGTGCCTTTCAGATTCACAGCC 423
 Db 648 ACCTTTTCAGAGCACTTATAGAGCATGACGAAATGCGGGTCTCTGCAAGTTCACACC 707
 QY 424 ATCGGCTGCTCGAGAGCTGAGAGGTGAGAACAGCAGAGCAGAGTGCAGTGGCTG 483
 Db 708 GTTGGCTTTTCAGAGATGTGAGACTGAGAACCTCAGAGTATGAGCTGAGCGGCTA 767
 QY 484 CGGAGCACTGGCCATGCTACTGAGCTCGTGTGGAGGCAAGCCCTCTTTGGAGAGC 543
 Db 768 CGGGAACACTAGCCCTACTGCTGAGCTCATCTTGGAGGCCCAAGCTCTCCAGAGACC 827
 QY 544 CAGAGCAGCGGGGTACAGCTCTGAGAGGTGCGAGAGCTGGAGAGAGAGAGCGCC 603
 Db 828 TTGAACAGGTGGGGCCAGAGCTACTCCAGCGGTGCCAGATTTTGAGAGAGAGATAGCA 887
 QY 604 ACTTTTGAACAATTCTCGCTCTGAAACCGGAGGTGGAGAGGTGGCCATGACTGCC 663
 Db 888 ACCTTTGAGAACATTTCTGCTGCTTGAACCTGAGTAGAGAGGTGAGCTGACTGCA 947
 QY 664 GAGGCTGAGCGGCGAGCAGCGGTGGACCAAGAACAGATTGAAGCCCTGAGTAGCAAG 723
 Db 948 GAGGCTTGTAGCGGCGAGCAGCGGTGAGACCAAGATTGAGGCCCTGAGTAAACAAG 1007
 QY 724 GTGCAGCACTGAGAGAGGACATGGCCCTCAGAGGACCTGGCATGGCTGACTTGGAGGAG 783
 Db 1008 GTGCACACCTGAGAGAGGAGCTGCGCCCTCAGAGGACCTGGCATGGCTGACTTGGAGGAG 1067
 QY 784 AAGGCTTTGGAGATGAGGACATCCACTACGATGGGCTCTTCATCTGGAAGATCTCAGAC 843
 Db 1068 AAGGCTCCGAGTTGGAAGTATCCACTATGATGGGCTCTTCATCTGGAAGATCTCTGAC 1127
 QY 844 TTGCGCCAGAGACTCCAGAGAGTGTGGCTGGCGCATACCCGCCATCTTCTCCCGAGCC 903
 Db 1128 TTACACAGAAAGCGTCAGAGAGCGGTGAGCTGGCGGACACCAAGCTATCTTCTCCCGAGCC 1187
 QY 904 TTCTACACAGAGGTACCGGCTACAGATGTGTCTGCGTATCTACTGAAACCGGACCGCC 963
 Db 1188 TTCTACACAGAGATATGGCTACAGATGTGTCTACGAGTCTACTTGAATGGCGAGCGC 1247
 QY 964 ACCGGCGAGGAAACACACTGTCTCTTCTTTGTGGTGAATGAAGGCCCGAATGACGCC 1023
 Db 1248 ACTGGCGGGGAACTCATCTGTCTCTTCTTCTGTTGATGAAAGGCCCAATGATGT 1307
 QY 1024 CTGCTCGGTGGCCCTTCAACAGAGGTGACCTTAATGCTGCTGACACAGAAATACCGG 1083
 Db 1308 CTGTTGAGTGGCTTTTAACTGAAAGGTAAATTAATGTTGCTGGAACCTAACACCGG 1367
 QY 1084 GAGCAGTGAATGAGCCCTTCAGGCCCGGACGTGACTTCACTCTTTTCAGAGGCCAGTC 1143
 Db 1368 GAGCATGTGATCGAGCAATTCAGGCCCGGATGAACCTGCTCTCTTTCAGAGGCCCTGTC 1427
 QY 1144 AACGACATGACATCGAGAGCGGTGCGCCCTCTTCTGCGCCGTCTCCAGAGATGAGGCA 1203
 Db 1428 AGTGACATGAACATCGCCAGTGGCTGCGCCCTCTTCTGCGCCGTGTGTCAGAGATGAGGCC 1487
 QY 1204 AAGAAATTCCTACGTGGGAGACGATGCACTCTTCATCAAGGCCATTTGTGAACCTGACAGG 1263
 Db 1488 AAGAAATTCCTATGTGGGGATGATGGAATCTTCATCAAGAGCTATTGTGAGCCTAACAGGA 1547
 QY 1264 CTCTA 1268
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Db 1548 CTCTA 1552
 RESULT 7
 US-10-085-117-330
 ; Sequence 330, Application US/10085117
 ; Publication No. US2003023334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: 529452000121
 ; CURRENT APPLICATION NUMBER: US/10/085,117
 ; CURRENT FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 09/798,586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 330
 ; LENGTH: 1251
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-085-117-330
 Query Match 23.4%; Score 296.6; DB 15; Length 1251;
 Best Local Similarity 66.2%; Pred. No. 2.1e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
 QY 586 CTGAGAGAGAGAGCGCCACTTTTGAACAATTTCTGCTGACCTGAAACCGGAGGTGGAG 645
 Db 568 CTGAGGGGAGAGCTGCTGTGTTTGAACAATTTGCTGCTCTTCAACAAGGAGGTGGAG 627
 QY 646 AGGTTGCCATGACTGCGAGGGCTGCAGCGGCGAGCACCAGGTGGACCAAGAGATT 705
 Db 628 GCCTCCACCTGGCCCTGGCCACCTCTATCCACAGAGCCAGCTGGACCGTGGAGCGCATC 687
 QY 706 GAAGCCCTGAGTAGCAGAGTGCAGCAGCTGGAGAGAGCATTGGCCCTCAGAGGACCTGGCG 765
 Db 688 CTGAGCTTGGAGCAGAGGGTGGTGGAGCTTCAGCAGACCCCTGGGCCCAAGAACCCAGGCC 747
 QY 766 ATGCTGCACTTGGAGCAGAGAGGTCTTGGAGATGGAGGATCCACCTACGATGGGGTCTTC 825
 Db 748 CTGGCAAGCTGGAGCAGAGAGCTTGGCGCTCATGGAGGAGGCGCTCTTCGATGGCACTTTC 807
 QY 826 ATCTGGAAGATCTCAGACTTGGCGAGGAAGCTCCAGGAAGCTGTGGCTGGCGCGCATACCC 885
 Db 808 CTGTGGAAGATACCAATGTACCCAGCGGTGCCATGAGTCCGCGCTGTGGCAGACCGTC 867
 QY 886 GCCATCTTCCCGCAGCGCTTCTACACAGCAGAGTACGGCTACAAGATGTCTGCGTATC 945
 Db 868 AGCTCTTCTCCCGCAGCGCTTCTACCTGCGCAAGTATGGCTACAAGTTGCGCTGCGGCTG 927
 QY 946 TACTGAACCGCGCAGCGCACCGGCGAGGAAACAACACTGTGCTCTTCTTTTGGTGGATG 1005
 Db 928 TACTGAATGGAGATGGCACTGGAAAGAGAAACCACTGTGCTCTTCTATCGTGTATCATG 987
 QY 1006 AAGGGCCGATGACGCCCTGCTGCGGTGGCGCTTCAACCCAGAGGTGACCTTAATGCTG 1065
 Db 988 AGAGGGAGTATGATGCGCTGCTGCGCGCTTTCAGCGCTTCCGGCGCTGACCTTAAGCTCAG 1047
 QY 1066 CTCACACAGAAATACCGGAGCAGCTGATTTGAGCGCTTTCAGGCGCGACGCTGACTTCATCC 1125
 Db 1048 CTGACCCAGAACACCTGAGCAGCGCTTTCAGCGCTTCCGGCGCTGACCTTAAGCTCAGCG 1107
 QY 1126 TCTTTTCAGAGGCGAGTCAACGACATGAACATGCAAGCGGTGCGCCCTCTTCTGCGCCC 1185
 Db 1108 TCTTTCAGAGGCGCGCAGAGTGAACCAACAGCTGGCCAGTGGATGCCACTCTTCTTCCCC 1167
 QY 1186 GTCTCCCAAGATGGAGCA---AAGAAATTCCTAGCTGGCGGACGATGCCATCTTTCATCAAG 1242
 Db 1168 CTAGCAAACTGCACTCACCACAGCAGCGCTACGTGAAGGACGACAAATGTTCTCTCAAG 1227
 QY 1243 GCCATTGTGGA 1253
 |||||

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Db 1228 TGCATTGTGGA 1238
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US-10-067-125-1
; Sequence 1, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR FILING DATE: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 1
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (76)..(1326)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: U19261 Genbank
; DATABASE ENTRY DATE: 1995-02-21
US-10-067-125-1

Query Match 23.4%; Score 296.6; DB 14; Length 2380;
Best Local Similarity 66.2%; Pred. No. 2.5e-76;
Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGAGAGAAAGACGGCCACTTTTGAACAATTTCTGCGCTCTGAACCGGGAGGTGGAG 645
Db 643 CTGAGGGGAAAGTCGGTGTGTTTGAACAATTTCTGCTCTCAACAAGAGGTGGAG 702
QY 646 AGGCTGGCCATGATCGCGAGCGCTGAGCGGAGACCGGCTGGACCAAGACAGATT 705
Db 703 GCCTCCCACTTGGCCCTGCGCCACTCTATCCAGAGCGAGCTGGACCTGAGCGCATC 762
QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTGGCG 765
Db 763 CTGAGCTTGGAGCAGAGGCTGGTGGAGCTTCAGCAGACCTTGGCCCGAAGACAGGCC 822
QY 766 ATGCTGACTTGGAGCAGAGGCTTGGAGATGGAGGATCCACCTAGATGGGGTCTTC 825
Db 823 CTGGGCAAGCTGGAGCAGAGCTTGGCCCTATGAGAGAGGCTCTCTTCGATGGCACTTC 882
QY 826 ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGGCTGGCCGATACCC 885
Db 883 CTGTGGAAGATCACCAGTGTCCAGCGCGGTGCCATGATGCTGGCTTGGCAGGACCGTC 942
QY 886 GCCATCTTCTCCAGCGCTTACACAGAGGATCGGCTACAAAGATGTGTCTCGGTATC 945
Db 943 AGCCTCTTCTCCCGAGCTTACACTGCCAAGTATGGCTACAAAGTGTGTGCTCGGCTG 1002
QY 946 TACTGAAACGCGAGCGGACCGGCGAGGACACACCTGCTCTCTTCTTGTGTGATG 1005
Db 1003 TACTGTAATGAGATGGCATGTGGAAGAGAACCCATCTGTCTCTTATCGTATCATG 1062
QY 1006 AAGGCGCGAATACGCCCTCTCGGTGGCCCTTCAACAGAGGATGACCTTAAATGCTG 1065
Db 1063 AGAGGGAGTATGATGCTGCTGCGCTGGCCCTTCGGAAACAGGTCACCTTCATGCTG 1122
QY 1066 CTCAGCAGATACCGGAGCAGCTGATGAGCCTTCAGGCCCGACGTCATCTATCC 1125
Db 1123 CTGACCAAGAAACCGTGAGCAGCCATTGACCCCTTCGGCTGACCTTAAGCTCAGG 1182
QY 1126 TCTTTTTCAGAGGCCAGTCAACGACATGAACATCGAAGCGGCTGCCCCCTCTTCTGCCCC 1185
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Db 1183 TCCTTCCAGAGCCCCCAGAGTGAAACCAACGTGGCCAGTGGCCACTTCTTCTCCCC 1242
QY 1186 GTCTCCAAGATGGAGGCA---AAGAAATTCCTACGTGCGGGAGCATGCCATCTTCAATCAAG 1242
Db 1243 CTCAGCAAACTGCAGTCAACCAAGCAGCCTACGTGAAGGAGCAGACAAATGTTCTCAAG 1302
QY 1243 GCATTGTGGA 1253
Db 1303 TGCATTGTGGA 1313
|||||
RESULT 9
US-10-172-118-1184
; Sequence 1184, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR FILING DATE: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1184
; LENGTH: 2380
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005658
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1184

Query Match 23.4%; Score 296.6; DB 15; Length 2380;
Best Local Similarity 66.2%; Pred. No. 2.5e-76;
Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

QY 586 CTGAGAGAAAGACGGCCACTTTTGAACAATTTCTGCGCTCTGAACCGGGAGGTGGAG 645
Db 643 CTGAGGGGAAAGTCGGTGTGTTTGAACAATTTGTTGCTCTCAACAAGAGGTGGAG 702
QY 646 AGGCTGGCCATGATCGCGAGCGCTGAGCGGAGACCGGCTGGACCAAGACAGATT 705
Db 703 GCCTCCCACTTGGCCCTGCGCCACTCTATCCAGAGCGAGCTGGACCTGAGCGCATC 762
QY 706 GAAGCCCTGAGTAGCAAGGTGACAGCTGGAGAGGAGCATTTGGCCCTCAAGGACCTGGCG 765
Db 763 CTGAGCTTGGAGCAGAGGCTGGTGGAGCTTCAGCAGACCTTGGCCCGAAGACAGGCC 822
QY 766 ATGCTGACTTGGAGCAGAGGCTTGGAGATGGAGGATCCACCTAGATGGGGTCTTC 825
Db 823 CTGGGCAAGCTGGAGCAGAGCTTGGCCCTATGAGAGAGGCTCTCTTCGATGGCACTTC 882
QY 826 ATCTGGAAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGGCTGGCCGATACCC 885
Db 883 CTGTGGAAGATCACCAGTGTCCAGCGCGGTGCCATGATGCTGGCTTGGCAGGACCGTC 942
QY 886 GCCATCTTCTCCAGCGCTTACACAGAGGATCGGCTACAAAGATGTGTCTCGGTATC 945
Db 943 AGCCTCTTCTCCCGAGCTTACACTGCCAAGTATGGCTACAAAGTGTGTGCTCGGCTG 1002
QY 946 TACTGAAACGCGAGCGGACCGGCGAGGACACACCTGCTCTCTTCTTGTGTGATG 1005
Db 1003 TACTGTAATGAGATGGCATGTGGAAGAGAACCCATCTGTCTCTTATCGTATCATG 1062
QY 1006 AAGGCGCGAATACGCCCTCTCGGTGGCCCTTCAACAGAGGATGACCTTAAATGCTG 1065
Db 1063 AGAGGGAGTATGATGCTGCTGCGCTGGCCCTTCGGAAACAGGTCACCTTCATGCTG 1122
QY 1066 CTCAGCAGATACCGGAGCAGCTGATGAGCCTTCAGGCCCGACGTCATCTATCC 1125
Db 1123 CTGACCAAGAAACCGTGAGCAGCCATTGACCCCTTCGGCTGACCTTAAGCTCAGG 1182
QY 1126 TCTTTTTCAGAGGCCAGTCAACGACATGAACATCGAAGCGGCTGCCCCCTCTTCTGCCCC 1185
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QY 1006 AAGGCCCCGAATGACGCCCTGCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG 1065
 Db 1063 AGAGGGAGTATGATGCGTGTGCGTGGCCCTTCCGGAACAAGGTACCTTCAATGCTG 1122
 QY 1066 CTCGACCAAGTAACCGGGAGCAGCTGATTGAGCCCTTCAGGCCCGGACGCTGACTTCATCC 1125
 Db 1123 CTGACCAAGTAACCGGTGAGCAGCCATTGACGCCCTTCGCGCTGACCTAAGCTCAGG 1182
 QY 1126 TCTTTTCAGAGCCAGTCAAGCAATGACATGCGAAGCGGTGCGCCCTCTTCTGCCCC 1185
 Db 1183 TCCTTCCAGAGGCCAGAGTGAACCAACGTTGGCCAGTGGATGCCCACTCTTCTTCCCC 1242
 QY 1186 GTCTCAAGATGAGGCA--AAGAACTCTAGTGGGAGAGATGCCATCTTCATCAAG 1242
 Db 1243 CTGACCAACTGAGTCAACCCAGCAGCTAGTGAAGAGACACAAATGTTCTCAAG 1302
 QY 1243 GCCATTGTGA 1253
 Db 1303 TGCATTGTGA 1313

RESULT 10

US-10-085-117-329
 ; Sequence 329, Application US/10085117
 ; Publication No. US2003023234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
 ; FILE REFERENCE: 52945200121
 ; CURRENT APPLICATION NUMBER: US/10/085,117
 ; CURRENT FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 09/798,586
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 361
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 329
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-085-117-329

Query Match 23.4%; Score 296.6; DB 15; Length 2380;
 Best Local Similarity 66.2%; Pred. No. 2.5e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
 QY 586 CTGAGAAAGAGCGCCACTTTTGAGAACATTGCTGCTGCTGAACCGGAGGTGGAG 645
 Db 643 CTGAGGGGAGCTGGTGTGTTGAGAACATTGCTGCTCAACAGAGGTGGAG 702
 QY 646 AGGTGGCCATGACTGCCGAGGCTTGCAGCGGAGCAGCCGCTGACCAAGCAAGATT 705
 Db 703 GCCTCCACCTGGCCCTGACCTCTATCCAGAGCCAGCTGGACCGTGAAGCATC 762
 QY 706 GAAGCCCTGAGTACCAAGGTGACAGCTGGAGAGGAGCATTTGCCCTCAAGAGCTTGG 765
 Db 763 CTGAGCTTGGAGCAGAGGTGGTGGAGCTTTCAGAGACCTTGCCTCAACAGAGGTGGAG 822
 QY 766 ATGGCTGACTTGGAGCAGAGGTCTTTGGAGATGGAGGATCCACCTACGATGGGGTCTTC 825
 Db 823 CTGGCAAGCTGGAGCAGAGGTTCGCGCTCATGGAGAGGCTCTCTTCGATGGCACTTTC 882
 QY 826 ATCTGGAGATCTCAGACTTCGAGGAGCTTCCAGGAAAGCTCCAGGAAAGCTGTGGTGGCCGATACCC 885
 Db 883 CTGTGGAAGATCAACCAATGTCACAGCGGTGTCATGATGGCGCTGTGGAGAGCCGTC 942
 QY 886 GCATCTTCTCCCGAGCTTCTACACAGCAGGTAGCGGTACAAAGATGTGTCTGGGTATC 945
 Db 943 AGCTCTTCTCCCGAGCTTCTACATGCGCAAGTATGGCTACAGTTGTGCTCGGCTG 1002
 QY 946 TACCTGAACGGCAGCGGAGCGGAGGAAACACACTGTGCTCTTCTTCTTGTGATG 1005
 Db 1003 TACCTGAATGAGATGGCACTGGAAGAGAACCCATCTGTGCTCTTCTATCGTATCATG 1062

RESULT 11

US-10-342-887-1184
 ; Sequence 1184, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 10/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 1184
 ; LENGTH: 2380
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-1184

Query Match 23.4%; Score 296.6; DB 16; Length 2380;
 Best Local Similarity 66.2%; Pred. No. 2.5e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
 QY 586 CTGAGAAAGAGCGCCACTTTTGAGAACATTGCTGCTGCTGAACCGGAGGTGGAG 645
 Db 643 CTGAGGGGAGCTGGTGTGTTTGAAGAACATTGCTGCTCAACAGAGGTGGAG 702
 QY 646 AGGTGGCCATGACTGCCGAGGCTTGCAGCGGAGCAGCCGCTGACCAAGCAAGATT 705
 Db 703 GCCTCCACCTGGCCCTGGCCACCTCTATCCAGAGCCAGCTGGACCGTGAAGCATC 762
 QY 706 GAAGCCCTGAGTACCAAGGTGACAGCTGGAGAGGAGCATTTGCCCTCAAGAGCTTGG 765
 Db 763 CTGAGCTTGGAGCAGAGGTGGTGGAGCTTTCAGAGACCTTGCCTCAACAGAGGTGGAG 822
 QY 766 ATGGCTGACTTGGAGCAGAGGTCTTGGAGATGGAGCATCCACCTACGATGGGGTCTTC 825
 Db 823 CTGGCAAGCTGGAGCAGAGGTTCGCGCTCATGGAGAGGCTCTCTTCGATGGCACTTTC 882
 QY 826 ATCTGAAGATCTCAGACTTCGAGGAGCTTCCAGGAAAGCTCCAGGAAAGCTGTGGTGGCCGATACCC 885

Db 883 CTGTGGAAGATCAACCAATGTACACAGGCGGTGCCATGATGCTGGCGCTGTGGCAGACCGTC 942
 QY 886 GCCATCTTCTCCCAAGCCTTCTACACAGCAGGTACCGCTACAAAGATGTGTCTGCGTATC 945
 Db 943 AGCCTCTTCTCCCAAGCCTTCTACACTGCCAAGTATGGCTACAAAGTTGTGCTGCGGCTG 1002
 QY 946 TACCTGAACGCGGACGCGGACCGGAGGACACACCTGTCCCTTCTTGTGTGATG 1005
 Db 1003 TACCTGAATGGAGATGGCACTGGAAAGAACCATCTGTCTCTTCTCATGATCATG 1062
 QY 1006 AAGGCGCCGAATGAGCGCCCTCTGCGGTGGCCCTTCAACCAAGAGGTGACCTTAATCTG 1065
 Db 1063 AGAGGGAGTATGATGCGCTGCTGCGGTGGCCCTTCCGAAACAGGTACCTTCATGCTG 1122
 QY 1066 CTCGACCAAGATACCGGAGCAGTGTGATGACGCTTCAGGCGCGGAGCTGACTTCATCC 1125
 Db 1123 CTGGACCAAGAACACCGTGAGCAGCCATTGACGCTTCCGCGCTGACCTAAGCTCAGCG 1182
 QY 1126 TCTTTTCAGAGCCAGTCAACGACATGAACATCGAAGCGGCTGCCCGCTCTTCTGCCCC 1185
 Db 1183 TCTTTCCAGAGCCCGCAGAGTGAACCAACGTCGAGTGGATGCCCACTTCTTCCCC 1242
 QY 1186 GTCTCCAGATGGAGGCA---AAGAAATCTTACGTGGGAGCAGTGCATCTTCATCAAG 1242
 Db 1243 CTCAGCAAACTGCAGTCAACCAAGCAGCCTACGTGAAGGACGACACAATGTTCTCTCAAG 1302
 QY 1243 GCCATTGTGGA 1253
 Db 1303 TGCATTGTGGA 1313

RESULT 12
 US-10-044-090-823
 ; Sequence 823, Application US/10044090
 ; Publication No. US20020137081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Olga Bandman
 ; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
 ; FILE REFERENCE: PA-0028 US
 ; CURRENT FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 823
 ; LENGTH: 5981
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20020137081A1 228001.3
 US-10-044-090-823

Query Match 23.4%; Score 296.6; DB 13; Length 5981;
 Best Local Similarity 66.2%; Pred. No. 3.1e-76;
 Matches 444; Conservative 0; Mismatches 224; Indels 3; Gaps 1;
 QY 586 CTGAGAGAGACGCGCCACTTTGAGACATTTCTGCGCTCTGAGCCGCGAGGTGGAG 645
 Db 1265 CTGAGGGAAGAGTGGGTGTTTGAACATTTGCTGTCTCTCAACAGAGGTGGAG 1324
 QY 646 AGGTGGCCATGATCGCGAGCCTGACGCGGAGCAGCAGCGGTGGACCAAGACAAGATT 705
 Db 1375 GCCTCCCACTGGCCCTGTGCCACCTCTATCCACAGAGCCAGCTGGACCGTGAGCGCATC 1384
 QY 706 GAAGCCCTGATAGCAAGTGCAGAGCTGAGAGAGCAATTTGCGCTCAAGGACCTGGCG 765
 Db 1385 CTGAGCTTGGAGCAGAGGCTGGTGGAGCTTCAGCAGACCCCTGGCGCCCAAGAACAGCGCC 1444
 QY 766 ATGGCTGACTTGGAGCAGAAAGGTCTTGAGATGAGGATCCTCACTACGATGGGCTTTC 825
 Db 1445 CTGGCAAGCTGGAGCAGAGCTTGGCGCTCATGAGAGGCGCTCTTCGATGGCACTTTC 1504

QY 826 ATCTGAGATCTCAGACTTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCGCATACCC 885
 Db 1505 CTGTGGAAGATCACAATGTACACAGGCGGTGCCATGATGAGTGGCGCTGTGGCAGACCGTC 1564
 QY 886 GCCATCTTCTCCCAAGCCTTCTACACAGCAGGTACCGCTACAAAGATGTGTCTGCGTATC 945
 Db 1565 AGCCTCTTCTCCCAAGCCTTCTACACTGCCAAGTATGGCTACAAAGTTGTGCTGCGGCTG 1624
 QY 946 TACCTGAACGCGGACGCGGACCGGAGGACACACCTGTCCCTTCTTGTGTGATG 1005
 Db 1625 TACCTGAATGGAGATGGCACTGGAAAGAACCCATCTGTCTCTTCTCATGATCATG 1684
 QY 1006 AAGGCGCCGAATGAGCGCCCTCTGCGGTGGCCCTTCAACCAAGAGGTGACCTTAATCTG 1065
 Db 1685 AGAGGGAGTATGATGCGCTGCTGCGGTGGCCCTTCCGAAACAGGTACCTTCATGCTG 1744
 QY 1066 CTCGACCAAGATACCGGAGCAGTGTGATGACGCTTCAAGCGCTTCAGGCGCGAGCTGACTTCATCC 1125
 Db 1745 CTGGACCAAGAACACCGTGAGCAGCCATTGACGCTTCCGCGCTGACCTAAGCTCAGCG 1804
 QY 1126 TCTTTTCAGAGCCAGTCAACGACATGAACATCGCAAGCGGCTGCCCGCTCTTCTGCCCC 1185
 Db 1805 TCTTTCCAGAGCCCGCAGAGTGAACCAACGTCGAGTGGATGCCCACTTCTTCCCC 1864
 QY 1186 GTCTCCAGATGGAGGCA---AAGAAATCTTACGTGGGAGCAGTGCATCTTCATCAAG 1242
 Db 1865 CTCAGCAAACTGCAGTCAACCAAGCAGCCTACGTGAAGGACGACACAATGTTCTCTCAAG 1924
 QY 1243 GCCATTGTGGA 1253
 Db 1925 TGCATTGTGGA 1935

RESULT 13
 US-10-453-478-7
 ; Sequence 7, Application US/10453478
 ; Publication No. US20030208043A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
 ; Jian Ni and Jing-Shan Hu
 ; TITLE OF INVENTION: Human Genes, Sequences and
 ; Expression Products
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CECCHIA, BYRNE, BAIN, GILFILLAN,
 ; CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/453,478
 ; FILING DATE: 04-Jun-2003
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/705,771
 ; FILING DATE: August 30, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MULLINS, J.G.
 ; REGISTRATION NUMBER: 33,073
 ; REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 973-994-1700
 ; TELEFAX: 973-994-1744
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2361 base pairs

QY	766	ATGGCTGACTTGGAGCAGAGGTCTTGGAGATGAGGATCCACCTACGATGGGGTCTTC	825
Db	727	CTGGCAGCTTGGACACAGTCTCGACTCATGAGGAGGATCCTTTGATGGTACTTTC	786
QY	826	ATCTGGAAGATCTCAGACTTCCGAGGAAGCTCCAGGAAGCTGTGGTGGCCGATACCC	885
Db	787	CTGTGGAAGATCACCAATGTCAACAAGCGGTGCCACGAGTCAGTGTGTGGCCGACTGTC	846
QY	886	GCCATCTTCTCCCGAGCCTTCTACACGACGAGTACGGCTACAGATGTGTCTGCGTATC	945
Db	847	AGCCTCTTCTCTCAGCTTCTACCTGCCAAGTATGTTACAAAGTTGTGCTGCGCTTG	906
QY	946	TACCTGAACGGCGAGCGCACCGGGCGAGGAACACACCTGTCCCTCTTCTTTTGGTGATG	1005
Db	907	TACCTGAACGGGGATGGCTCAGGCAAGAAGACCCACCTGTCCCTCTTTCATCGTGATCATG	966
QY	1006	ANGGCCCCGATGACGCCCTGCTGGGTGGCCCTTCAACAGAGGTGACCTTAATGCTG	1065
Db	967	AGAGGAGAAATACGATGCTCTCTGCTGGCCTTTCAGGAACAAGGTACCTTTATGCTA	1026
QY	1066	CTCGACCAGAAATAACCGGGAGCAGTGTGATTGACGCTTTCAGGCCCGACGTCACCTTCATCC	1125
Db	1027	CTTGACCAAGAACACCGAGAGCATGCTATTGATGCTTCCGGCCTGACCTGAGCTCAGCC	1086
QY	1126	TCTTTTCAGAGCCAGTCAACGACATGAACATCGCAAGCGGTGCCCCCTCTTCTGCCCCC	1185
Db	1087	TCCTTCCAGCGGCCACAGAGTGAGACCAACGTTGGCCAGCGGCTGCCGCTCTTCTTCCCC	1146
QY	1186	GTCTCCAAAGATGGAGGCA--AAGAAATTCCTACGTGGGGACGATGCCATCTTTCATCAAG	1242
Db	1147	CTCAGCAAGCTGCAGTCAACCCAGCAGCCTACGTCAAAGATGACACAAATGTTCTCTCAA	1206
QY	1243	GCCATTTGGGAC	1254
Db	1207	TGCATTGTGGAC	1218

Search completed: November 6, 2004, 23:46:30
Job time : 707 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 18:54:26 ; Search time 4401 Seconds
(without alignments)
10507.162 Million cell updates/sec

Title: US-10-018-030B-1

Perfect score: 1269

Sequence: 1 atggctgcagctagctgac.....tggacctgacagggctctaa 1269

Scoring table: IDENTITY NUC

Gapop 10_0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1020.4	80.4	2193	3	CR611225	full-length
2	802	63.2	918	5	BU553823	AGENCOURT
3	771.6	60.8	857	4	EG877004	602623643
4	769	60.6	906	5	EX329304	EX329304
5	701	55.2	2993	3	AK052934	Mus muscu
6	699.4	55.1	2116	3	AK038136	Mus muscu
7	695	54.8	1506	9	AY413598	Homo sapi
8	647.8	51.0	668	6	CD630731	560712757
9	646.2	50.9	666	6	CD630730	560712758
10	631.4	49.8	934	5	BU857656	AGENCOURT
11	577.2	45.5	937	5	BU513753	AGENCOURT
12	573.2	45.2	578	4	BM790399	K-EST0070
13	498.6	39.3	1335	9	AY413599	Pan trogl
14	488	38.5	710	7	CK596664	AGENCOURT
15	486.2	38.3	495	2	AW882089	RC6-OT005
16	483.6	38.1	979	6	CB181509	AGENCOURT
17	453.4	35.7	881	5	EX370491	EX370491
18	447.6	35.3	551	2	BE683286	182742 MA
19	444.4	35.0	1506	9	AY413600	Mus muscu
20	439	34.6	835	7	CO566760	AGENCOURT
21	438.8	34.6	686	7	CK948654	4073760 B
22	437.4	34.5	1082	5	BX395088	BX395088
23	435.8	34.3	489	6	CB112836	K-EST0154
24	431.2	34.0	1073	1	AL526829	AL526829

25	427.8	33.7	855	7	CO574786	CO574786
26	427.2	33.7	585	7	CN432957	BEQ30005A
27	425.2	33.5	629	7	CO573496	AGENCOURT
28	422.4	33.3	603	1	AA619651	V101F10.1
29	412.4	32.5	442	4	EG326688	602410937
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33	399.2	31.5	640	7	CK944910	4069342 B
34	388.2	30.6	481	2	BF775206	285298 MA
35	388.2	30.6	513	5	BQ305196	MRO-BT200
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38	372	29.3	477	2	BF775207	285299 MA
39	369	29.1	465	6	CB133303	K-EST0184
40	367.6	29.0	587	5	BP872066	BP872066
41	367.6	29.0	639	7	CN345159	170004705
42	367.6	29.0	729	4	EG385770	602454002
43	367.6	29.0	795	5	EX424592	EX424592
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45	367.6	29.0	879	4	BI093667	602859992

ALIGNMENTS

RESULT 1
LOCUS CR611225 2193 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODK009YH01 of HeLa cells Cot 25-normalized of Homo sapiens (human).
ACCESSION CR611225
VERSION CR611225.1 GI:50492032
KEYWORDS HTC; CNSUT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2193)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue
REFERENCE 2 (bases 1 to 2193)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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QY 1 ATGGCTGCAGCTAGCTGACCCCCCTGGCTCCCTGGAGTTGCTACAGCCCGGCTTCTCC 60
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QY	515 TGTCTGAGGCAAGCCCTCTTTGGAGACACAGAGCACGCGGGTTCAGAGCTCTCGAGA 574 	
DB	121 TGTCTGAGGCAAGCCCTCTTTGGAGACACAGAGCACGCGGGTTCAGAGCTCTCGAGA 180 	
QY	575 GGTGCGAGAGCTGGAGAGAGAGACGGCCACTTTTGAGAACTTGTCTGCGCTCTGAACC 634 	
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QY	635 GGGAGGTGAGAGGGTGGCCATGACTGCGAGGCTTCAGCGCGGAGCACCGGTGAGCC 694 	
DB	241 GGGAGGTGAGAGGGTGGCCATGACTGCGAGGCTTCAGCGCGGAGCACCGGTGAGCC 300 	
QY	695 AAGACAGATTGAGCCCTGAGTACGAGTGCAGAGTGCAGAGTGCAGAGGAGCATTTGSCCTCA 754 	
DB	301 AAGACAGATTGAGCCCTGAGTACGAGTGCAGAGTGCAGAGTGCAGAGGAGCATTTGSCCTCA 360 	
QY	755 AGGACCTGGCGATGGCTGACTTTGGAGCAGAAGGTCTTGAGATGAGGACATCCACCTACG 814 	
DB	361 AGGACCTGGCGATGGCTGACTTTGGAGCAGAAGGTCTTGAGATGAGGACATCCACCTACG 420 	
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QY	875 GCGCATACCGGCATCTTCTCCCGACGCTTCTACACAGCAGGTACGGCTACAGATGT 934 	
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DB	541 GTCTGGATATCTACCTGAACAGCGCAGCGCACCGGGGAGGAAACACACCTGTCCCTTTCT 600 	
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QY	1055 CCTTAATGTCTGTCGACCAAGAAATAACGGGAGACAGTGAATGACCCCTTCAGGCCCGGAG 1114 	
DB	661 CCTTAATGTCTGTCGACCAAGAAATAACGGGAGACAGTGAATGACCCCTTCAGGCCCGGAG 720 	
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DB	721 TGACTTCATCTCTTTTCAGAGCCAGTCAAGACATGAACATCCAGACGCGCTGCCCC 780 	
QY	1173 CCTCTTCTGCCCCGTCTCCAAGAT-GGAGCGCAAGAAATTCCTACGT-GCGGACGATGCC 1230 	
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RESULT 3	BG677004 857 bp mRNA linear EST 01-MAY-2001	
LOCUS	602623643f1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:474855 5',	
DEFINITION	mRNA sequence.	
ACCESSION	BG677004	

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

6 (bases 1 to 2993)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 Location/Qualifiers
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FEATURES
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 Qy 361 TAGCA----- 365
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 Qy 366 ----- 365
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QY 301 GAGAGCTGCGGCGGTCTGTCCCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 360 GAGAGCTGCCAGCTGTCTGTCCCAATGATGATGATGATGATGATGATGATGATGATGATG 419

QY 361 TACGA----- 365
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[illegible]

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VERSION CD630731.1 GI:40278997
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 668)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
Location/Qualifiers
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ACCESSION CD630730
VERSION CD630730.1 GI:40278996
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 666)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com
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DB 486 CTTGGAGAAAGACCGGCCACTTTTGGAGAACATTTGCTGGCTCTCTGAACCGGGAGGTGA 427
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DB 426 GAGGGTGGCCATGACTCCGAGGCTCGAGCCGACACCGGCTGGACCAAGACAGAT 367
QY 705 TGAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGACATTTGGCTCAAGGACCTGGC 764
DB 366 TGAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGACATTTGGCTCAAGGACCTGGC 307
QY 765 GATGGCTGACTTGGAGCAGAAAGTCTTTGGAGATGGAGGATCCACCTACGATGGGCTCTT 824
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QY 825 CATCTGGAAGATCTCAGACTTTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCCGATACC 884
DB 246 CATCTGGAAGATCTCAGACTTTCGCCAGGAAGCTCCAGGAAGCTGTGGCTGGCCGATACC 187
QY 885 CGCCATCTTCCCGACCTTCTACACACGACGATACGGCTACAAGATGTGTCTGGGTAT 944

ORIGIN									
Query Match		45.5%	Score 577.2;	DB 5;	Length 937;				
Best Local Similarity		80.3%	Pred. No. 1.5e-128;						
Matches		689;	Conservative	0;	Mismatches	168;	Indels	1;	Gaps
QY	366	GTTCAGGACCAAGTCAAGACTTGTGCAAGTGTGAGTCCCTTCAGATTCACAGCCAT	425						
DB	45	GTTCAGGACCAATGTTAGAGCATGACGAAATGCGGGTTCCTGAGATTCACACCGT	104						
QY	426	CGGCTGCTCGAGACGGTAGAGGTGAGAAACAGCAGGACGAGAGTGCAGTGGCTGG	485						
DB	105	TGGCTGTTACAGAGATGTTGAGACTGAGAACTGAGAGATCATGAGTCGACGGCTAG	164						
QY	486	GGAGCACTGGCCATGCTACTGAGTCTGGTCTGGAGGCAAGCCCTCTTGGGAGACCA	545						
DB	165	GGAAACCTAGCCCTACTGCTGAGTCAATCTTGGAGGCCCAAGCCTCTCCAGGAACCTT	224						
QY	546	GAGCCACGGGGTTCAGAGCTCTCTGACAGAGTGGCAGAGCCTGGAGAAAGACGGCCAC	605						
DB	225	GAACAGGTGGGCCAGAGCTACTCCAGCGTGGCCAGATTTGGAGCAGAGATAGCAAC	284						
QY	606	TTTTGAGAACATTTGCTGCTGCTGAAACCGGAGAGTGGAGAGGTGGCCATGACTGCCGA	665						
DB	285	CTTTGAGAACATTTCTGCTGCTTTGAACCGTGAAGTAGAGAGGTAGCACTGACTGCAGA	344						
QY	666	GGCTTCAGCCGGCAGCACCGCTGGAACAGACAGATTGAAGCCCTGAGTAGCAAGT	725						
DB	345	GGCTTTAGCCGGCAGCACCGCTAGACCAAGATTTAGGSCCTGAGTAAACAGGT	404						
QY	726	GCACAGCTGGAGAGGAGCATTTGGCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAA	785						
DB	405	GCAACAGCTGGAGAGGAGCATCGGCTCAAGGACCTGGCATGGCTGACTGGAGCAGAA	464						
QY	786	GGTCTTGGAGATGGAGCATCCACTACGATGGGTCTTCATCTGGAAGATCTCAGACTT	845						
DB	465	GGTCTCCGAGTTGAAGTATCCACCTATGATGGGTCTTCATCTGGAAGATCTCTGACTT	524						
QY	846	CGCCAGGAAGCTCCAGGAAGCTGTGGTGGCCGCATACCCGCCATCTTCTCCCGAGCCTT	905						
DB	525	CACCAGAAAGCTCAGGAAGCCGTAGCTGGCCGGACACCAAGTATCTTCTCCCGAGCCTT	584						
QY	906	CTACACAGCAGGTACGGCTACAAGATGTGTCTGCTATCTACCTGAACGGCGACGGCAC	965						
DB	585	CTACACAGCAGATATGGCTACAAGATGTGTCTACGAGTCTACTTGAATGGCGACGGCAC	644						
QY	966	CGGCGAGGAACACACTGTCCTCTCTTTGTTGGTGAAGGGCCCGCAATGACGGCCT	1025						
DB	645	TGGCGGGGAACTCATCTGCTCTCTCTCTTCGTTGGTGAAGAGGCCCAATGATGCTCT	704						
QY	1026	GCTCGGTTGGCCCTTCAACAGAGAGGTGACCTTAATGCTGCTCGACCAAGATAACCGGGA	1085						
DB	705	GTTGCAGTGGCTTTTAAATCAGAGGTAAACATTGATGTTGCTGGGACATAACCCCGGA	764						
QY	1086	GCAGTGATTGAGCCTTCAGGCCGACGAGTCACTTCCTCTTTTCAGAGGCCAGTCAA	1145						
DB	765	GCATGTGATCGACGCATTCAGGCGCCGATGACCTGCTCTCTTCCAGAGGCCCTGTCAG	824						
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DB	825	TGACATGAACATCGCCCAAGTGGCTGGCCCCCTCTCTGCCCCCTGGTCCCAGATGAGGGCA	884						
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DB	885	AGAAATCTATGGGGCGG 902							
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LOCUS									
DEFINITION K-RST0070221 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-8-D01									
5', mRNA sequence.									
ACCESSION BM790399									

RESULT 12
 BM790399 578 bp mRNA linear EST 05-MAR-2002
 LOCUS K-EST0070221 S22SNU16n1 Homo sapiens cdna clone S22SNU16n1-8-D01
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 ACCESSION BM790399

BM790399.1 GI:19138631		EST.		Homo sapiens (human)	
SOURCE		Homo sapiens		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 578)		Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.B., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.	
AUTHORS		21C Frontier Korean EST Project 2001		Unpublished (2002)	
TITLE		Genome Research Center		Korea Research Institute of Bioscience & Biotechnology	
JOURNAL		52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea		Tel: +82-42-860-4470	
COMMENT		Fax: +82-42-860-4409		Email: yongsung@mail.kribb.re.kr	
		Plate: 8 row: D column: 01		High quality sequence stop: 578.	
FEATURES		Location/Qualifiers		1..578	
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ORIGIN		Query Match		45.2%; Score 573.2; DB 4; Length 578;	
		Best Local Similarity		99.5%; Pred. No. 1.3e-127;	
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QY	629	TGAACCGGAGGTGAGAGGTGGCCATGACTGCGAGGCTGCGAGCGGAGCAGCAGCGGC	688		
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QY	689	TGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGAGCATTTG	748		
DB	61	TGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCAGCAGCTGGAGAGGAGCATTTG	120		
QY	749	GCCTCAAGAGCTGGCGATGCTGACTGGAGCAGAGGTCTTGGAGATGAGGAGCATCCA	808		
DB	121	GCCTCAAGAGCTGGCGATGCTGACTGGAGCAGAGGTCTTGGAGATGAGGAGCATCCA	180		
QY	809	CCTACGATGGGCTCTTCACTGGAAGATCTCAGACTTGCAGGAAGTCCAGGAAGCTGCCAGGAAGCTG	868		
DB	181	CCTACGATGGGCTCTTCACTGGAAGATCTCAGACTTGCAGGAAGTCCAGGAAGCTGCCAGGAAGCTG	240		
QY	869	TGGCTGGCGGATATCCCGCCATCTTCCCGAGCTTCTACACGAGGAGTACGGCTACA	928		
DB	241	TGGCTGGCGGATATCCCGCCATCTTCCCGAGCTTCTACACGAGGAGTACGGCTACA	300		
QY	929	AGATGTGTCTGGTATCTACCTGAACGGCGAGCGCACCGGGCGAGGAACACACCTGTCTCC	988		
DB	301	AGATGTGTCTGGTATCTACCTGAACGGCGAGCGCACCGGGCGAGGAACACACCTGTCTCC	360		
QY	989	TCTTCTTTGTGTGATGAAGGGCCCGCCCTGCTGCGGTGGCTCTTCAACACGAGA	1048		

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Db      361  TCTTCTTTGCTGATGAAGGCGCCGATGAGCCCTGCTGGGTGGCCCTTCAACAGA 420
Qy      1049  AGGTGACCTTAATGCTGTCGACCAAGATAACCGGAGACAGTGAATGACCCCTTCAGGC 1108
Db      421  AGGTGACCTTAATGCTGTCGACCAAGATAACCGGAGACAGTGAATGACCCCTTCAGGC 480
Qy      1109  CCGAGTGAATTCATCTCTTTTCAGAGCCAGTCAACGACATGAACATCGAAGCGCT 1168
Db      481  CCGAGTGAATTCATCTCTTTTCAGAGCCAGTCAACGACATGAACATCGAAGCGCT 540
Qy      1169  GCCCCTCTTCTGCCCCGCTCCCAAGATGGAGGCAAG 1206
Db      541  GCCCCTCTTCTGCCCCGCTCCCAAGATGGAGGCAAG 578

RESULT 13
LOCUS   AY413599
DEFINITION Pan troglodytes TRAF2 gene, linear GSS 17-DEC-2003
GENOMIC SURVEY SEQUENCE
ACCESSION AY413599.1 GI:39769561
VERSION   1
KEYWORDS  GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1335)
AUTHORS  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
          gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 1335)
AUTHORS  Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (18-NOV-2003) Celera Genomics, 45 West Gude Drive,
          Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
          them based on alignment.
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          Qy      83  TGGAGCCAGTACTGTGCTCCGCTGCAAGAACGTCCTCCGACAGCCCTTCAGGCGC 142
          Db      61  TGGAGCCAGTACTGTGCTCCGCTGCAAGAACGTCCTCCGACAGCCCTTCAGGCGC 120
          Qy      143  AGTGTGCCACCGGTACTGTCTCTTCTGCTGGCCAGCATCCTCAGCTCTGGGCTTCAGA 202
          Db      121  AGTGTGCCACCGGTACTGTCTCTTCTGCTGGCCAGCATCCTCAGCTCTGGGCTTCAGA 180

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Qy      203  ACTGTCTGCTGTGTTTCAGAGGGCATATATGAAGAGGCAATTTCTATTTTAGAAAGCA 262
Db      181  ACTGTCTGCTGTGTTTCAGAGGGCATATATGAAGAGGCAATTTCTATTTTAGAAAGCA 240
Qy      263  GTTTCGGCCTTCCAGATAATGCTGCCCGCAGGAGGTGGAGAGCCTGCCGCGCTCTGTC 322
Db      241  GTTCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 300
Qy      323  CAGTGAATGATGCACTGGAAGGGGACCTGAAAGAAATACG----- 364
Db      301  CCAGTGAATGATGCACTGGAAGGGGACCTGAAAGAAATACGAGAGCTGCCACGAGGCC 360
Qy      365  ----- 364
Db      361  GCTGCCCGCTCATGCTGACTGAATGCTCCCGCTGCAAGGGCCTGGTCCGCTTGGTGA 420
Qy      365  ----- 364
Db      421  AGGAGCGCCACCTGGAGCACGAGTGCCTGGAGAGAACCTGAGCTGCCGGCATTGCCGG 480
Qy      365  ----- 364
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Qy      365  -----AGTTTCAGGACCAACGCTCAAGA 385
Db      541  CTTGTGACGGCTGCGGCAAGAAAGATCCCGCGGAGAGTTTCAGGACCAACGCTCAAGA 600
Qy      386  CTTGTGGCAAGTGTGAGTCCCTTCAGATTCACAGCCATCGGCTGCCTCGAGACGCTAG 445
Db      601  CTTGTGGCAAGTGTGAGTCCCTTCAGATTCACAGCCATCGGCTGCCTCGAGACGCTAG 660
Qy      446  AGGSGTGAAGAAACAGCAGGACGAGTGCAGTGGCTGCGGAGCACCTGCGCATGTCTAC 505
Db      661  AGGSGTGAAGAAACAGCAGGACGAGTGCAGTGGCTGCGGAGCACCTGCGCATGTCTAC 720
Qy      506  TGAGTCTGGTGTGAGGCAAGCCCTTCTGGGAGACCAAGCCACGCGGGGTGAGAGC 565
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Qy      566  TCCTCAGAGGTGCGAGAGCCTGGAGAGAGAGAGCGCCACTTTTGAGAACATCTCTGCG 625
Db      781  TCCTCAGAGGTGCGAGAGCCTGGAGAGAGAGAGCGCCACTTTTGAGAACATCTCTGCG 840
Qy      626  TCCTGAACCGGAGGTGGAGAGGTGGCCATGACTGCGAGGCGCTGAGCCCGGAGCACC 685
Db      841  TCCTGAACCGGAGGTGAGAGGTGGCCATGACTGCGAGGCGCTGAGCCCGGAGCACC 900
Qy      686  GGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAAGGTGACAGCTGAGAGGAGCA 745
Db      901  GGCTGGACCAAGACAGATTGAAGCCCTGAGTAGCAAGGTGAGTAGCAAGGTGAGAGG 960
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Db      1021  NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1080
Qy      866  CTGTGGCTGGCGCATACCCGCCATCTTCTCCAGCCTTCTACACAGCAGGTACGGCT 925
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Db      1261 NNNNGTGACCTTAAGTCTCTCGACAGAATAACCGGAGCAGTGATTGACGCGCTTCA 1320
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Db      1321 GGCCCGACGTGACTT 1335

RESULT 14
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LOCUS   AGENCOURT 17837571 NIH MGC 238 Rattus norvegicus cDNA clone
DEFINITION
IMAGS: 7131710 5', mRNA sequence.
CK596664
VERSION CK596664.1 GI:41109747
KEYWORDS EST.
SOURCE  Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 710)
           NIH-MGC http://mgi.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Contact: Daniela S. Gerhard, Ph.D.
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgabs-k@mail.nih.gov
           Tissue Procurement: Howard Jacobs
           cDNA Library Preparation: Express Genomics
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM15032 row: p column: 12
           High quality sequence stop: 585.
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     /notes="Organ: testis; Vector: pExpress-1; Site: 1: EcoRV;
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     animal. Tissues were snap-frozen and kept at -80C before
     RNA extraction and purification (Tri-reagent method). cDNA
     was primed using oligo-dT primer:
     5'-pGACTAGTCTAGATCGGAGCGCGCCGCTT25-3' and cloned into
     the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
     resulted in an average insert size of 1.9 kb. This primary
     library is normalized (non-normalized primary library is
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     (Frederick, MD)"

ORIGIN
Query Match      38.5%; Score 488; DB 7; Length 710;
Best Local Similarity 84.3%; Fred. No. 5.3e-107;
Matches 573; Conservative 0; Mismatches 105; Indels 2; Gaps 2;

QY      555 GGCGTCAGAGCTCCTCGAGAGGTGCGAGAGCCTGGAGAGAGACGGCCACATTGAGAA 614
Db      2 GGCGCCAGAGCTTTACAGCGGTGCCAGATTGAGAGAGAGAGACGACCTTTGAGNA 61.

QY      615 CATTGTCGTGCTCCTGAACCGGAGGTGGAGAGGGTGGCCATGCTGCGAGGCGCTGCGAG 674
Db      62 CATTGTCGTGCTTTGAACCGGAGGTAGAGAGGGTAGCAGTGAAGTCTGCTGAGAGGCTTTGAG 121

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QY      675 CCGGAGACACCGGCTGGACCAAGACAAGATTGAAGCCCTGAGTAGCAAGGTGCGAGCAGCT 734
Db      122 CCGGAGACACCGGCTGAGACCAAGACAAGATTGAAGCCCTAAGACCAAGGTGCGAGCAGCT 181
QY      735 GGAGAGGAGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAGAGGCTTTGGA 794
Db      182 GGAGAGGAGCATTGGCCTCAAGGACCTGGCGATGGCTGACTTGGAGCAGAGAGGCTTTGGA 241
QY      795 GATGAGGAGCATCCACCTACGATGGGGTCTTTCATCTGGAAGATCTCAGACATTCGCGAGAA 854
Db      242 GTTGGAGGTGCCACCTATGATGGGTCTTTCATCTGGAAGATCTCCGACTTCGCGAGAA 301
QY      855 GCTCCAGGAAGCTGTGGCTGCGGCATACCGCCATCTTCTCCCGACGCTTCTACACAG 914
Db      302 ACGTCAGGAAGCATGCGCTGCGCGACACCTGCTATCTTCTCCCGACGCTTCTTCAAG 361
QY      915 CAGGTACGGCTACAGATGTGTCTGCGTATCTACTGAAACGGCGACGCGACGGCGGAGG 974
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QY      975 AACACACCTGCTCCTCTTCTTTGGTGATGAAGGGCCGGAATGACGCCCTGCTGCGGTG 1034
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QY      1035 GCCCTTCAACAGAGGTGACCTTAAATGCTCTCGACAGAAATAACCGGAGCAGCTGAT 1094
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QY      1215 CGTGGCGGACGATGCCATCT 1234
Db      660 CGTGGCGGATGACGCCATCT 679

RESULT 15
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LOCUS   RC6-OT0050-230200-021-B06 OT0050 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AW882089
VERSION   AW882089.1 GI:8044099
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 495)
AUTHORS  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
          Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
          Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
          Brunstein,A., Golliveira,P.S., Bucher,P., Jongeneel,C.V.,
          O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
          Simpson,A.J.
          Shotgun sequencing of the human transcriptome with ORF expressed
          sequence tags
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
          20202663
          10737800
          Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome

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Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC6-OT0050-230
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 Seq primer: puc 18 forward
 High quality sequence start: 9
 High quality sequence stop: 397.
 Location/Qualifiers

FEATURES

1..495
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 /note="Organ: ovary; Vector: puc18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match 38.3%; Score 486.2; DB 2; Length 495;
 Best Local Similarity 99.2%; Pred. No. 1.4e-106;
 Matches 488; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 632 ACCGGAGGTGGAGAGGTGCCATGACTGCCGAGGCTGCAGCCGCGAGCAGCGGTGG 691
 DB |||||
 QY 692 ACCAGACAAAGATTGACCCCTGAGTACGAGGTGCAGCAGCTGAGAGGAGCATGGCC 751
 DB |||||
 QY 64 ACCAGACAAAGATTGACCCCTGAGTAGCAAGGTGCAGCAGCTGAGAGGAGCATGGCC 123
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 DB |||||
 QY 124 TCAAGGACCTGGCGATGACTGACTTGGAGCAGAAAGGTCTTGGAGATGGAGGCATCCACCT 183
 DB |||||
 QY 812 ACGATGGGGTCTTCATCTGGAGATCTCAGACTTCGCCAGGAGCTCCAGGAGCTGTGG 871
 DB |||||
 QY 184 ACGATGGGGTCTTCATCTGGAGATCTCAGACTTCGCCAGGAGCTCCAGGAGCTGTGG 243
 DB |||||
 QY 872 CTGGCCGCATACCCGCCATCTCTCCCGAGCTTCTACACGAGGATACGGCTACAAGA 931
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 QY 932 TGTGTCTCGGTATCTACTGAAACGGGACCGCACCGGGCGAGGAAACACACTGTCTCCCTCT 991
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 QY 304 TGTGTCTCGGTATCTACTGAAACGGGACCGCACCGGGCGAGGAAACACACTGTCTCCCTCT 363
 DB |||||
 QY 992 TCTTTGTGGTATGAAGGGCCCGAATGACGCCCTGTGCGGTGGCCCTTCAACCCAGAGG 1051
 DB |||||
 QY 364 TCTTTGTGGTATGAAGGGCCCGAATGACGCCCTGTGCGGTGGCCCTTCAACCCAGAGG 423
 DB |||||
 QY 1052 TGACCTTAATCTGCTCGACAGAAATACCGGGAGCAGTGAATGAGCCCTTCAGGCCCG 1111
 DB |||||
 QY 424 TGACCTTAATCTGCTCGACAGAAATACCGGGAGCAGTGAATGAGCCCTTCAGGCCCG 483
 DB |||||
 QY 1112 ACGTGACTTCAT 1123
 DB |||||
 QY 484 ACGTGACTTCAT 495

Search completed: November 6, 2004, 22:02:17
 Job time : 4410 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2004, 16:10:49 ; Search time 155 Seconds
(without alignments)
976.669 Million cell updates/sec

Title: US-10-018-030b-2
Perfect score: 2211
Sequence: 1 MAASVTPGSELLQPGFS.....NSVYRDAIFKAIIVDLTGL 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2211	100.0	422	4 AAY71901	Aay71901 Human TRA
2	2047.5	92.6	501	3 AAY98165	Aay98165 Human TRA
3	2047.5	92.6	501	4 AAY71903	Aay71903 Human TNF
4	2047.5	92.6	501	6 ABO07170	AbO07170 Human p53
5	2047.5	92.6	501	7 ADB80956	Adb80956 RING-SH C
6	2047.5	92.6	501	7 ABR4599	Abr4599 TRAF2 pro
7	2047.5	92.6	501	8 ADM45822	Adm45822 TNF-alpha
8	1914.5	86.6	501	5 ABB57335	Abb57335 Mouse isc
9	1909.5	86.4	501	2 AAR30578	Aar30578 Mouse TRA
10	1751	79.2	336	4 AAY71902	Aay71902 Human TRA
11	1631.5	73.8	447	6 ADA54134	Ada54134 Human pro
12	1178	53.3	243	3 AAB07002	Aab07002 Human TRA
13	999.5	45.2	326	6 ABU07084	Abu07084 Human adi
14	733.5	33.2	416	2 AAU03147	Aau03147 Epstein-B
15	733.5	33.2	416	3 AAY98164	Aay98164 Human TRA
16	733.5	33.2	416	7 ADF76476	Adf76476 Novel hum
17	733.5	33.2	416	8 ADL22912	Adl22912 Human PR2
18	733.5	33.2	416	8 ADL82947	Adl82947 Human PRO
19	733.5	33.2	416	8 ADO20499	Ado20499 Human PRO
20	733.5	33.2	416	8 ADO19524	Ado19524 Human PRO
21	730	33.0	567	5 AAO17756	Aao17756 Murine CD
22	727	32.9	409	2 AAR30577	Aar30577 Human TRA
23	722	32.7	543	2 AAW27432	Aaw27432 Human TRA
24	722	32.7	543	6 ABO07169	AbO07169 Human p53
25	722	32.7	665	2 AAW27433	Aaw27433 Human TRA

ALIGNMENTS

RESULT 1
AAY71901

ID AAY71901 standard; protein; 422 AA.

XX AAY71901;

DT 26-MAR-2001 (first entry)

DE Human TRAF2 splice variant TRAF2TR (TRAF2 truncated) protein.

KW Human; tumour necrosis factor; TNF; TRAF2-FL; inhibitor; treatment;
KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
KW anti-inflammatory; cardiant; myocardial infarction; splice variant;
KW vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
KW rheumatoid arthritis; immunosuppressive; Crohn's disease; psoriasis;
KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW neurodegenerative disease.

XX Homo sapiens.

PN WO200066737-A1.

XX 09-NOV-2000.

PF 06-APR-2000; 2000WO-US009178.

PR 30-APR-1999; 99US-0131940P.

PA (AVET) AVENTIS PHARM PROD INC.

PI Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;

XX WPI: 2001-007223/01.

DR N-PSDB; AAO1947.

XX New nucleic acid encoding variants of tumor necrosis factor receptor
PT associated factors useful for inhibiting tumor necrosis factor alpha-
PT regulated pathways, and for treating Crohn's disease, psoriasis, and
PT rheumatoid arthritis.

PS Claim 5; Fig 2b; 74pp; English.

XX The present sequence is a tumour necrosis factor (TNF)-receptor
CC associated factor-truncated (TRAF2TR) protein which inhibits TNF alpha-
CC regulated pathways. This sequence is a natural splice variant of human
CC TRAF2-FL (full-length) protein. The TRAF2TR variant is useful for
CC inhibiting diseases involving overproduction of TNFalpha, TNFalpha

Aaw27436 Human CRA
Aaw27437 Human CRA
Abb57054 Mouse isc
Aaw27431 Human TRA
Aay98166 Human TRA
Aao17757 Human CD4
Adb80964 RING-SH C
Adb80957 RING-SH C
Aar98833 CD40 asso
Aar98833 Human TRA
Aaw03146 LMPI asso
Aao07171 Human p53
Aaw27434 Human CRA
Aar99259 Full-length
Aab67615 Amino aci
Adb25542 Binding d
Abu89708 Protein d
Aaw29258 Human TRA
Aaw27610 Human TRA

CC pathologies involving hyperactivation of nuclear factor kappa B (NFkB).
 CC The variant is also useful for inhibiting and treating inflammatory
 CC processes involving TNFalpha such as Crohn's disease, psoriasis,
 CC rheumatoid arthritis, graft versus host disease, non-insulin dependent
 CC diabetes, inflammatory bowel disease, and neurodegenerative diseases or
 CC cardiovascular disease such as cardiac ischaemia-reperfusion injury
 CC following myocardial infarction, coronary artery bypass surgery, cardiac
 CC transplantation or ischaemia-reperfusion injury in the central nervous
 CC system (CNS) following stroke, the progression and rupture of advanced
 CC coronary atherosclerotic plaques, development and progression of
 CC congestive heart failure, endothelial cell injury following balloon
 CC angioplasty, or apoptotic cell death of myocardial cells
 XX
 SQ Sequence 422 AA;
 Query Match 100.0%; Score 2211; DB 4; Length 422;
 Best Local Similarity 100.0%; Pred. No. 1.9e-207;
 Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAASVTPPGSLELLQPGFSKTLGKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 DB 1 MAASVTPPGSLELLQPGFSKTLGKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 QY 61 ILSSGPQCAACVHEGIEEGISILESSAPPDNAAREVESLPAVCPDGTWKGLKE 120
 DB 61 ILSSGPQCAACVHEGIEEGISILESSAPPDNAAREVESLPAVCPDGTWKGLKE 120
 QY 121 YEFQDHVTCGKCRVPCRFHAIAGCLETVEGSKQEHVQMLREHLAMLLSVLEAKPLG 180
 DB 121 YEFQDHVTCGKCRVPCRFHAIAGCLETVEGSKQEHVQMLREHLAMLLSVLEAKPLG 180
 QY 181 DOSHAGSLELLQRCESLEKKTATFENIVCNLREVERVAMTAACRSRHRDQDKIEALSS 240
 DB 181 DOSHAGSLELLQRCESLEKKTATFENIVCNLREVERVAMTAACRSRHRDQDKIEALSS 240
 QY 241 KVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISDFAPKLOEAVAGRIPIAFSP 300
 DB 241 KVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISDFAPKLOEAVAGRIPIAFSP 300
 QY 301 AFYTSRYGKMKCLRIYINGDGTGRGTHLSLFFVVMKGPNDALLRPFNQKVTMLDQNN 360
 DB 301 AFYTSRYGKMKCLRIYINGDGTGRGTHLSLFFVVMKGPNDALLRPFNQKVTMLDQNN 360
 QY 361 REHVIDAFRPDVTSSSFQRPVNDNMNIASGCLFCFVSKMEAKNSYVRDDAIFIKAIVDLT 420
 DB 361 REHVIDAFRPDVTSSSFQRPVNDNMNIASGCLFCFVSKMEAKNSYVRDDAIFIKAIVDLT 420
 QY 421 GL 422
 DB 421 GL 422
 RESULT 2
 AA98165
 ID AA98165 standard; protein; 501 AA.
 AC AA98165;
 DT 30-AUG-2000 (first entry)
 DX Human TRAF2 protein sequence.
 DE
 XX Tumour necrosis factor receptor-associated factor; TRAF; human;
 KW antisense oligonucleotide; phosphorothioate; antiproliferative;
 KW anti-inflammatory; B-selectin; jun kinase.
 XX
 OS Homo sapiens.
 XX
 PN WO200020435-A1.
 PD 13-APR-2000.
 PP 05-OCT-1999; 99WO-US023171.
 PF

XX 06-OCT-1998; 98US-00167109.
 PR (ISIS-) ISIS PHARM INC.
 XX Baker BF, Cowser LM, Monia BP, Xu XS;
 PI WPI; 2000-303732/26.
 DR N-PSDB; AAA55491.
 XX Antisense oligonucleotides targeted to nucleic acids encoding human tumor
 PT necrosis factor receptor-associated factor (TRAF); useful for treating
 PT diseases associated with TRAF expression such as inflammatory diseases.
 XX
 PS Disclosure; Page 109-111; 170pp; English.
 XX The present invention relates to antisense oligonucleotides (see AAA55496
 CC -A55757) which are targeted to nucleic acids encoding a human tumour
 CC necrosis factor receptor-associated factor (TRAF). The antisense
 CC sequences comprise at least one modified internucleotide linkage, which
 CC is a phosphorothioate linkage. The oligonucleotides also include at least
 CC one modified sugar moiety such as a 2'-O-methoxyethyl sugar moiety.
 CC Sequences AAA55490-A55495 represent nucleotide sequences encoding human
 CC TRAF1-6, and sequences AA98164-98169 represent the TRAF1-6 amino acid
 CC sequences. Included in the invention is a method for treating a human
 CC having a disease associated with the expression of TRAF comprising
 CC administering an antisense oligonucleotide. The reduction of jun kinase
 CC activation in cells comprises contacting the cells with an antisense
 CC oligonucleotide targeted to TRAF-6. A method for the reduction of B-
 CC selectin expression in cells or tissues comprises contacting the cells or
 CC tissues with an antisense oligonucleotide targeted to TRAF-2 or TRAF-6.
 CC The antisense oligonucleotides have antiproliferative and anti-
 CC inflammatory activity and are useful for treating disorders associated
 CC with cell proliferation and inflammation. The antisense oligonucleotides
 CC may also be used as a diagnostic probe for studying gene function
 XX
 SQ Sequence 501 AA;
 Query Match 92.6%; Score 2047.5; DB 3; Length 501;
 Best Local Similarity 80.4%; Pred. No. 2.6e-191;
 Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSKTLGKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 DB 1 MAASVTPPGSLELLQPGFSKTLGKLEAKYLCACRNVLRRPFAQCCHRYCSFCLAS 60
 QY 61 ILSSGPQCAACVHEGIEEGISILESSAPPDNAAREVESLPAVCPDGTWKGLKE 120
 DB 61 ILSSGPQCAACVHEGIEEGISILESSAPPDNAAREVESLPAVCPDGTWKGLKE 120
 QY 121 YE-----
 DB 121 YESCHEGRCPMLTBCPACKGLVRLGEXERHLEHECPERSLSRCHRAPCCGADVKAHHE 180
 QY 123 -----FQDHVTCGKCRVPCRFHAIAGCLETVEGSKQEHVQWL 161
 DB 181 VCPKFFLTCDGCGKKKIPREXFQDHVTCGKCRVPCRFHAIAGCLETVEGSKQEHVQWL 240
 QY 162 REHLAMLLSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCNLREVERVAMTA 221
 DB 241 REHLAMLLSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCNLREVERVAMTA 300
 QY 222 EACSRHRLDQDKIEALSSKVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISD 281
 DB 301 EACSRHRLDQDKIEALSSKVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISD 360
 QY 282 FARKLOEAVAGRIPIAFSPAFYTSRYGKMKCLRIYINGDGTGRGTHLSLFFVVMKGPND 341
 DB 361 IURKLOEAVAGRIPIAFSPAFYTSRYGKMKCLRIYINGDGTGRGTHLSLFFVVMKGPND 420
 QY 342 LLRWPFNQKVTMLDQNNREHVIDAFRPDVTSSSFQRPVNDNMNIASGCLFCFVSKMEAK 401
 DB 421 LLRWPFNQKVTMLDQNNREHVIDAFRPDVTSSSFQRPVNDNMNIASGCLFCFVSKMEAK 480

QY 402 KNSVVRDDAIFIKAVDLTGL 422
Db 481 KNSVVRDDAIFIKAVDLTGL 501

RESULT 3
AAV71903
ID AAV71903 standard; protein; 501 AA.
XX
AC AAV71903;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human TNF-receptor associated factor (TRAF2) protein.
XX
KW Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
KW TNF-receptor associated factor; TRAF2 truncated; TRAF2TR;
KW TRAF2 truncated-deleted; TRAF2TD; antiinflammatory; cardiac; vasotropic;
KW antiapoptotic; antirheumatic; antiarthritic; antidiabetic;
KW antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
KW rheumatoid arthritis; graft versus host disease; cardiovascular disease;
KW non-insulin dependent diabetes; inflammatory bowel disease; stroke;
KW neurodegenerative disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 2..87
FT /note= "This region is absent in TRAF2TD (AAV71902)"
FT Region 123..201
FT /note= "This region is absent in TRAF2TR (AAV71901) and
FT TRAF2TD (AAV71902)"
XX
PN WO200066737-A1.
XX
PD 09-NOV-2000.
XX
XX 06-APR-2000; 2000WO-US009178.
XX
XX 30-APR-1999; 99US-0131940P.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
XX Searfoss GH, Pagnoni MF, Ivashchenko YD, Guo K, Clark KL;
XX WPI; 2001-007223/01.
XX N-PSDB; AAD01949.
XX
XX New nucleic acid encoding variants of tumor necrosis factor receptor
XX associated factors useful for inhibiting tumor necrosis factor alpha-
XX regulated pathways, and for treating Crohn's disease, psoriasis, and
XX rheumatoid arthritis.
XX
XX Example 1; Fig 4b; 74pp; English.
XX
XX The present sequence is human tumour necrosis factor (TNF)-receptor
XX associated factor-full length (TRAF2-FL) protein. TRAF2-FL has two
XX variants, a splice variant of TRAF2 referred as "TRAF2 truncated"
XX (TRAF2TR) and a TRAF2 expression construct with enhanced dominant
XX negative properties referred as "TRAF2 truncated-deleted" (TRAF2TD).
XX TRAF2-TR and TRAF2-TD are also capable of inhibiting TNF alpha signalling
XX pathways. The TRAF2 variants are useful for inhibiting diseases involving
XX over production of TNFalpha, TNFalpha pathologies involving
XX hyperactivation of nuclear factor kappa B (NFkB). The variants are also
XX useful for inhibiting and treating inflammatory processes involving
XX TNFalpha such as Crohn's disease, psoriasis, rheumatoid arthritis, graft
XX versus host disease, non-insulin dependent diabetes, inflammatory bowel
XX disease, and neurodegenerative diseases or cardiovascular disease such as
XX cardiac ischaemia-reperfusion injury following myocardial infarction,
XX coronary artery bypass surgery, cardiac transplantation or ischaemia-
XX reperfusion injury in the central nervous system (CNS) following stroke,
XX the progression and rupture of advanced coronary atherosclerotic plaques,

CC development and progression of congestive heart failure, endothelial cell
CC injury following balloon angioplasty, or apoptotic cell death of
CC myocardial cells
XX
SQ Sequence 501 AA;
Query Match 92.6%; Score 2047.5; DB 4; Length 501;
Best Local Similarity 80.4%; Pred. No. 2.6e-191;
Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFAQCCHRYCSFCIAS 60
Db 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFAQCCHRYCSFCIAS 60
QY 61 ILSSGPQNCACVHEGIYEBGISTILESSAPPDNNARREVSLEPAVCPDCTWKGLKE 120
Db 61 ILSSGPQNCACVHEGIYEBGISTILESSAPPDNNARREVSLEPAVCPDCTWKGLKE 120
QY 121 YE----- 122
Db 121 YESCHEGRCPLMTECPACKGLVRLGKERHLEHECPERSLSRHCRAPCGADVKAHHE 180
QY 123 -----FQDHVKTGCKRVPFCRPHAIGCLETVEGEKQOEHEVQWL 161
Db 181 VCPKFPPLTCDGCGKKIPREXFQDHVKTGCKRVPFCRPHAIGCLETVEGEKQOEHEVQWL 240
QY 162 REHLAMLSSVLEAKPLLDQSHAGSELQRCESLEKKTATFENIVCVLNEVERVAMTA 221
Db 241 REHLAMLSSVLEAKPLLDQSHAGSELQRCESLEKKTATFENIVCVLNEVERVAMTA 300
QY 222 EACSRQHRLDQDKIEALSSKVQQLERSIGLKDAMADLEQXVLEMEASTYDGVFIWKISD 281
Db 301 EACSRQHRLDQDKIEALSSKVQQLERSIGLKDAMADLEQXVLEMEASTYDGVFIWKISD 360
QY 282 PARKLOEAVAGRIIPAISPAFTSYRYGKMLRILYNGDGTGRTGTHLSLFFVVMKGPDA 341
Db 361 ILRLQLEAVAGRIIPAISPAFTSYRYGKMLRILYNGDGTGRTGTHLSLFFVVMKGPDA 420
QY 342 LLRWPFNOKVTLMLLDQNNREHVIDAFRPDVTSSTSSFORPVNDNMNIASGCPDFCPSKNEA 401
Db 421 LLRWPFNOKVTLMLLDQNNREHVIDAFRPDVTSSTSSFORPVNDNMNIASGCPDFCPSKNEA 480
QY 402 KNSVVRDDAIFIKAVDLTGL 422
Db 481 KNSVVRDDAIFIKAVDLTGL 501

RESULT 4
AS007170
ID AB007170 standard; protein; 501 AA.
XX
AC AB007170;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human p53 modifying protein, SEQ ID 130.
XX
KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
KW apoptotic disorder; cell proliferation disorder.
XX
OS Homo sapiens.
XX
PN WO200299122-A1.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017382.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.

XX (EXEL-) EXELIXIS INC.
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 XX WPI; 2003-156859/15.
 XX N-PSDB; ACD13346.
 XX Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.
 XX Example 2; Page 431-432; 678pp; English.
 XX The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human orthologue of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence
 CC represents a human p53 pathway modifying protein
 XX Sequence 501 AA;
 XX
 XX Query Match 92.6%; Score 2047.5; DB 6; Length 501;
 XX Best Local Similarity 80.4%; Pred. No. 2.6e-191;
 XX Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSTLLGTLKLEAKYLCACNRVLRPFQACGCHRYCSFCLAS 60
 DB 1 MAASVTPPGSLELLQPGFSTLLGTLKLEAKYLCACNRVLRPFQACGCHRYCSFCLAS 60
 QY 61 ILSSGPQNCACVHEGIVEEGISILESSAPDPAARREVESLPVCPDGCTWKGLKE 120
 DB 61 ILSSGPQNCACVHEGIVEEGISILESSAPDPAARREVESLPVCPDGCTWKGLKE 120
 QY 121 YE----- 122
 DB 121 YESCHEGRCPLMLTECPACKGLVRLGEKERHLEHECPERSLSRCHRAPCCGADVAKAHE 180
 QY 123 -----FQDHVTKCGKRCVPCSFHAIGCLTVEGKQHEVQWL 161
 DB 181 VCPFPPLTDCGCKKKIPREFQDHVTKCGKRCVPCSFHAIGCLTVEGKQHEVQWL 240
 QY 162 REHLAMLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNERERVANTA 221
 DB 241 REHLAMLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNERERVANTA 300
 QY 222 EACSRQHLDDQKIEALSSKVOQLERSIGLKDLAMADLEQKVRPFQACGCHRYCSFCLAS 60
 XX

DB 301 EACSRQHLDDQKIEALSSKVOQLERSIGLKDLAMADLEQKVRPFQACGCHRYCSFCLAS 360
 QY 282 PARKLOEAVAGHPIAIFSPAFYTSRYGYKMCRLIYVINGGCTGRGTHLSLFFVWKGND 341
 DB 361 ILRLKOEAVAGHPIAIFSPAFYTSRYGYKMCRLIYVINGGCTGRGTHLSLFFVWKGND 420
 QY 342 LLRWPFNQKVTLMMLDDQNNREHVIDAFRPDVTSSSFQRPVNDMNIAASGCLFPCPVSKMEA 401
 DB 421 LLRWPFNQKVTLMMLDDQNNREHVIDAFRPDVTSSSFQRPVNDMNIAASGCLFPCPVSKMEA 480
 QY 402 KNSYVRDDAIFKAIKAVDLTGL 422
 DB 481 KNSYVRDDAIFKAIKAVDLTGL 501
 XX
 XX RESULT 5
 XX ADB80956
 XX ID ADB80956 standard; protein; 501 AA.
 XX AC ADB80956;
 XX DT 04-DEC-2003 (first entry)
 XX DE RING-SH complex related protein, SEQ ID No 30.
 XX KW RING-SH 3; Gag protein; Gag late domain; P13K; actin; myosin; Hsp60;
 XX Hsp70; Hsp90; STAM1; STAM2A; STAM2B; VHS-UIM; GTPase; E2 enzyme; tsG101;
 XX cullin; RING-SH; clathrin; virucide; vaccine; antiviral; retrovirus;
 XX rhabdovirus; filovirus.
 XX Unidentified.
 XX WO2003033646-A2.
 XX 24-APR-2003.
 XX 31-JUL-2002; 2002WO-US024589.
 XX 31-JUL-2001; 2001US-0308958P.
 XX 09-NOV-2001; 2001US-0345846P.
 XX (PROT-) PROTEOLOGICS INC.
 XX Greener T, Moskowitz H, Reiss Y, Alroy I;
 XX WPI; 2003-393509/37.
 XX N-PSDB; ADB80997.
 XX New isolated protein complex comprising a RING-SH 3 polypeptide and
 XX another polypeptide, useful for detecting cells infected with a virus,
 XX and for treating viral disorders caused by retroviruses, rhabdoviruses,
 XX or filoviruses.
 XX Disclosure; Fig 30; 176pp; English.
 XX The invention relates to a novel isolated protein complex comprising a
 XX RING-SH 3 polypeptide and a polypeptide selected from a Gag protein, a
 XX Gag late domain, P13K, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A,
 XX STAM2B, VHS-UIM, a GTPase, an E2 enzyme, tsG101, a cullin, RING-SH, and a
 XX clathrin. The novel protein complex has virucide activity and can be used
 XX to treat disorders as part of a vaccine. The protein complex and
 XX composition are useful for detecting cells infected with a virus, for
 XX identifying agents having antiviral activity, and for treating viral
 XX disorders caused by retroviruses, rhabdoviruses, or filoviruses. This
 XX sequence is a protein comprising the RING-SH complex of the invention.
 XX Sequence 501 AA;
 XX Query Match 92.6%; Score 2047.5; DB 7; Length 501;
 XX Best Local Similarity 80.4%; Pred. No. 2.6e-191;
 XX Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSTLLGTLKLEAKYLCACNRVLRPFQACGCHRYCSFCLAS 60

Db 1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRVCSFCLAS 60
 QY 61 ILSSGPONCAACVHEGIEYEGISILESSAFPDPNAARREVESLPVCPDQCTWKGTIKE 120
 Db 61 ILSSGPONCAACVHEGIEYEGISILESSAFPDPNAARREVESLPVCPDQCTWKGTIKE 120
 QY 121 YE----- 122
 Db 121 YSCHGRCPLMLTBCPACKGLVRLGKERHLEHPCPERSLSRCHRAPCCGADVKAHHE 180
 QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVGEGKQOEHEVQWL 161
 Db 181 VCPKPLTCDGCGKKKIPREKFQDHVKTGCKRVPFCRFAIGCLTVGEGKQOEHEVQWL 240
 QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
 Db 241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
 QY 222 EACSQRHLDDQKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 281
 Db 301 EACSQRHLDDQKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 360
 QY 282 FARKLOEAVAGRIPAFSPAFYTSRYGYKWCLEIYLNQDGTGRGTHLSLFFVVMKGPND 341
 Db 361 ILRKLOEAVAGRIPAFSPAFYTSRYGYKWCLEIYLNQDGTGRGTHLSLFFVVMKGPND 420
 QY 342 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 401
 Db 421 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 480
 QY 402 KNSYVRDDAIFIKAIVDLTGL 422
 Db 481 KNSYVRDDAIFIKAIVDLTGL 501

RESULT 6
 ABR84599
 ID ABR84599 standard; protein; 501 AA.
 AC
 XX ABR84599;
 DT 18-DEC-2003 (first entry)
 DE TRAF2 protein.
 XX
 KW TRAF2; inflammatory response; rheumatoid arthritis; LTBetaR;
 KW lymphotoxin-beta receptor; modulator; cancer; immunological disease;
 KW apoptosis; cytostatic; immunosuppressive; antirheumatic; antiarthritic;
 KW antiinflammatory; dermatological; nephrotropic; antithyroid;
 KW thymine; musclic; neuroprotective; antianemic; haemostatic;
 KW vasotropic; antidiabetic.
 XX
 OS Unidentified.
 XX
 PN WO2003066834-A2.
 PD 14-AUG-2003.
 XX
 PF 10-FEB-2003; 2003WO-US003923.
 XX
 PR 08-FEB-2002; 2002US-0355183P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Kuai J, Wooters JL, Nickbarg EB, Qiu Y, Lin L;
 DR WPI; 2003-748125/70.
 DR N-PSDB; ACF04633.
 XX
 PT New purified lymphotoxin-beta receptor protein complex, useful for
 PT identifying modulators of lymphotoxin-beta receptor activity or
 PT expression for treating or preventing cancer or an autoimmune disorder,

PT e.g. vasculitis or diabetes.
 XX Disclosure; Page 6; Opp; English.
 XX
 CC The present invention relates to a purified complex comprising a
 CC lymphotoxin beta receptor (LTbetaR) polypeptide and Smac polypeptide. The
 CC lymphotoxin-beta receptor (LTbetaR) complex is useful for identifying
 CC modulators of LTbetaR activity or expression for treating or preventing
 CC cancer or an immune disorder such as autoimmune disorder, e.g. rheumatoid
 CC arthritis, systemic lupus erythematosus, Goodpasture's syndrome, Grave's
 CC disease, Hashimoto's thyroiditis, pemphigus vulgaris, myasthenia gravis,
 CC scleroderma, autoimmune haemolytic anaemia, autoimmune thrombocytopenic
 CC purpura, polymyositis, dermatomyositis, pernicious anaemia, Sjogren's
 CC syndrome, ankylosing spondylitis, vasculitis, or type I diabetes
 CC mellitus. The present sequence is a TRAF2 protein, which forms part of
 CC the complex of the invention
 XX
 SQ Sequence 501 AA;

Query Match 92.6%; Score 2047.5; DB 7; Length 501;
 Best Local Similarity 80.4%; Pred. No. 2.6e-191;
 Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;
 QY 1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRVCSFCLAS 60
 Db 1 MAAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRPFOACGHRVCSFCLAS 60
 QY 61 ILSSGPONCAACVHEGIEYEGISILESSAFPDPNAARREVESLPVCPDQCTWKGTIKE 120
 Db 61 ILSSGPONCAACVHEGIEYEGISILESSAFPDPNAARREVESLPVCPDQCTWKGTIKE 120
 QY 121 YE----- 122
 Db 121 YSCHGRCPLMLTBCPACKGLVRLGKERHLEHPCPERSLSRCHRAPCCGADVKAHHE 180
 QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVGEGKQOEHEVQWL 161
 Db 181 VCPKPLTCDGCGKKKIPREKFQDHVKTGCKRVPFCRFAIGCLTVGEGKQOEHEVQWL 240
 QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
 Db 241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
 QY 222 EACSQRHLDDQKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 281
 Db 301 EACSQRHLDDQKIEALSKVQQLERSIGLKDLAMADLEQKYLEMASTYDGVFIWKISD 360
 QY 282 FARKLOEAVAGRIPAFSPAFYTSRYGYKWCLEIYLNQDGTGRGTHLSLFFVVMKGPND 341
 Db 361 ILRKLOEAVAGRIPAFSPAFYTSRYGYKWCLEIYLNQDGTGRGTHLSLFFVVMKGPND 420
 QY 342 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 401
 Db 421 LLRWPFNQKVTMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNTASGCPFCPVSKMEA 480
 QY 402 KNSYVRDDAIFIKAIVDLTGL 422
 Db 481 KNSYVRDDAIFIKAIVDLTGL 501

RESULT 7
 ADM45822
 ID ADM45822 standard; protein; 501 AA.
 XX
 AC ADM45822;
 XX
 DT 03-JUN-2004 (first entry)
 DE
 DE TNF-alpha receptor complex-related TRAF2 protein.
 KW protein complex; tumour necrosis factor alpha receptor; TNF-alpha; TNFR;
 KW nuclear factor; NF-kappaB activating kinase; NAK; RasGAP3;
 KW transducin repeat-containing protein; TRCP1; TRCP2; antiinflammatory;


```

Db 121 YESCHGELCPFLTECPACKGLVRLSEKHEHTTEQCPKRSLSQCHCAPSHVDLEVHYE 180
QY 123 -----FQDHVKTGCKRVPORFHAIGCLTVEGEKQOEHEVQWL 161
Db 181 VCPKPLTCDGCGKXKIPRETQDQHVACSKRVLRCFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLLSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 221
Db 241 REHLALLSFLAQSPGTLNQVGPQLLQRCILQEQKIATFENIVCVLNREVERVAMTA 300
QY 222 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKVELEASTYDGVFWKISD 281
Db 301 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKVELEASTYDGVFWKISD 360
QY 282 PARKLOEAVAGRIPAFSPAFYTSRYGYKMLRVLNGDGTGRGTHLSLFFVVMKGNDA 341
Db 361 FTRKQOAVAGRTPAFSPAFYTSRYGYKMLRVLNGDGTGRGTHLSLFFVVMKGNDA 420
QY 342 LLRWPFNQKVTMLLDQNNREHVIDAFRDPVTSSSFQRPVNDMNIASGCPLEFCPVSKMEA 401
Db 421 LLQWPFNQKVTMLLDHNNREHVIDAFRDPVTSSSFQRPVNDMNIASGCPLEFCPVSKMEA 480
QY 402 KNSYVRDDAIFKAIVDLTGL 422
Db 481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 9
AAR90578
ID AAR90578 standard; protein; 501 AA.
AC AAR90578;
DT 09-APR-1996 (first entry)
DE Mouse TRAF2.
KW TRAF2; tumour necrosis factor receptor associated factor 2; TNF; CD40.
OS Mus musculus.
FH Key Location/Qualifiers
FT Domain 272..501
FT Region 275..351
FT /label= TRAF_domain
FT /label= Leucine_zipper_region
XX WO9533051-A1.
XX 07-DEC-1995.
XX 25-MAY-1995; 95WO-US006639.
XX 27-MAY-1994; 94US-00250858.
XX 28-OCT-1994; 94US-00331394.
XX 22-MAY-1995; 95US-00446915.
XX (GETH ) GENENTECH INC.
XX Goeddel DV, Rothe M;
XX WPI; 1996-049310/05.
XX N-PSDB; AAT12262.
XX Tumour necrosis factor (TNF) receptor-associated factors - involved in
XX mediation of biological activities of TNF and CD40 ligands.
XX Claim 8; Page 75-76; 116pp; English.
XX Mouse tumour necrosis factor receptor associated factor 2 (TRAF2)
XX (AAR90578) is a new factor capable of specific association with the
XX intracellular domain of the type 2 TNF receptor (TNF-R2) and CD40, and is
```

```

CC involved in the mediation of TNF and CD40 ligand biological activities.
CC Recombinant TRAF2 is obt'd. by expression in host cells of a cDNA clone
CC (AAR12262) isolated using a yeast two-hybrid assay. It is used to
CC identify inhibitors of activities of TNF-R2, CD40 and/or LMP1 oncogene,
CC e.g. for treatment of endotoxic (septic) shock and rheumatoid arthritis
XX
SQ Sequence 501 AA;
Query Match 86.4%; Score 1909.5; DB 2; Length 501;
Best Local Similarity 74.1%; Pred. No. 8.8e-178;
Matches 371; Conservative 22; Mismatches 29; Indels 79; Gaps 1;
QY 1 MAASVTPPGSLELLQPGFKTLIGTLEAKYLCSACRNVLRRPFOACQCHRYCSFCLAS 60
Db 1 MAASVTPSPGSELELLQPGFKTLIGTLEAKYLCSACKNLRPFOACQCHRYCSFCLTS 60
QY 61 ILSSGPONCAACVHEGYIEGISESSAPFPDPAARREVESIPAVCPDGCCTWKGLKE 120
Db 61 ILSSGPQDCAACVIEGYIEGISESSAPFPDPAARREVESIPAVCPDGCCTWKGLKE 120
QY 121 YE----- 122
Db 121 YESCHGELCPFLTECPACKGLVRLSEKHEHTTEQCPKRSLSQCHCAPSHVDLEVHYE 180
QY 123 -----FQDHVKTGCKRVPORFHAIGCLTVEGEKQOEHEVQWL 161
Db 181 VCPKPLTCDGCGKXKIPRETQDQHVACSKRVLRCFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLLSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 221
Db 241 REHLALLSFLAQSPGTLNQVGPQLLQRCILQEQKIATFENIVCVLNREVERVAMTA 300
QY 222 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKVELEASTYDGVFWKISD 281
Db 301 EACSRQRLDQDKIEALSCKVQQLERSIGLKDAMADLEQKVELEASTYDGVFWKISD 360
QY 282 PARKLOEAVAGRIPAFSPAFYTSRYGYKMLRVLNGDGTGRGTHLSLFFVVMKGNDA 341
Db 361 FTRKQOAVAGRTPAFSPAFYTSRYGYKMLRVLNGDGTGRGTHLSLFFVVMKGNDA 420
QY 342 LLRWPFNQKVTMLLDQNNREHVIDAFRDPVTSSSFQRPVNDMNIASGCPLEFCPVSKMEA 401
Db 421 LLQWPFNQKVTMLLDHNNREHVIDAFRDPVTSSSFQRPVNDMNIASGCPLEFCPVSKMEA 480
QY 402 KNSYVRDDAIFKAIVDLTGL 422
Db 481 KNSYVRDDAIFKAIVDLTGL 501

RESULT 10
AAY71902
ID AAY71902 standard; protein; 336 AA.
AC AAY71902;
DT 26-MAR-2001 (first entry)
XX Human TRAF2TR variant, TRAF2 truncated-deleted (TRAF2TD) protein.
XX Human; tumour necrosis factor; TNF; TRAF2; inhibitor; treatment;
XX TNF-receptor associated factor; TRAF2 truncated-deleted; TRAF2TD;
XX antiinflammatory; cardiant; mutant; mutein; myocardial infarction;
XX vasotropic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic;
XX antiarteriosclerotic; immunosuppressive; Crohn's disease; psoriasis;
XX rheumatoid arthritis; graft versus host disease; cardiovascular disease;
XX non-insulin dependent diabetes; inflammatory bowel disease; stroke;
XX neurodegenerative disease; variant; TRAF2 truncated; TRAF2TR.
XX Homo sapiens.
XX Synthetic.
XX WO2000066737-A1.
XX
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```
QY 321 GTGGRGTHLSLFFVVMKGNDAIIRWPFNOKVTLMLLDQNNREHVIDAREPDTVTSSSFRP 380
DB 346 GTGGRGTHLSLFFVVMKGNDAIIRWPFNOKVTLMLLDQNNREHVIDAREPDTVTSSSFRP 405
QY 381 VNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 422
DB 406 VNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 447

RESULT 12
AAB07002
ID AAB07002 standard; protein; 243 AA.
XX AC
XX AAB07002;
XX
XX 17-OCT-2000 (first entry)
XX
XX Human TRAF2(NC)-CA21 protein.
XX
XX Human; TRAF(NC)-CA21 protein; Tumour-necrosis factor; TNF;
XX TNF receptor-associated factor; cell proliferation; cell differentiation;
XX apoptosis; inflammation; immune response; receptor-ligand binding assay.
XX
XX Homo sapiens.
XX
XX WO200026670-A1.
XX
XX 11-MAY-2000.
XX
XX 23-AUG-1999; 99WO-US019272.
XX
XX 29-OCT-1998; 98US-00181958.
XX
XX (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
XX Kehry MR, Pullen SS, Crute JJ;
XX
XX WPI; 2000-451628/39.
XX
XX Quantitative assay for measuring the effect of a substance on tumor
XX necrosis factor receptor associated factor protein interaction with it
XX receptor.
XX
XX Claim 7; Page 19-21; 27pp; English.
XX
XX Tumour necrosis factor (TNF) receptor has an important role in the
XX regulation of cellular proliferation, differentiation, and apoptosis in
XX inflammatory and immune responses. The present invention relates to a
XX quantitative assay for measuring the ability of a substance to effect
XX binding of a TNF receptor-associated factor (TRAF) protein to its
XX receptor. The present sequence is Human TRAF(NC)-CA21 protein fragment,
XX which was used in the present assay. This protein is the conserved C-
XX terminal region (NC) of TRAF2, and possesses a C-terminal tag that is
XX recognised by CA21 monoclonal antibody. Proteins which bind to the
XX present sequence are detected by CA21 antibody which generates a signal
XX
XX Sequence 243 AA;
XX
Query Match 53.3%; Score 1178; DB 3; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.5e-106;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 193 CESLEKKTATFENIVCVLNEVERVAMTAECRQHRDQDKTEALSSKVQQLERSIGLK 252
DB 1 CESLEKKTATFENIVCVLNEVERVAMTAECRQHRDQDKTEALSSKVQQLERSIGLK 60
QY 253 DLAMADLEQKVLMEASTDVGFIWIKISDFARKLQEAAGRIAPFSPAFYTSRYGYKVC 312
DB 61 DLAMADLEQKVLMEASTDVGFIWIKISDFARKLQEAAGRIAPFSPAFYTSRYGYKVC 120
QY 313 LRIYINGDGTGRGTHLSLFFVVMKGNDAIIRWPFNOKVTLMLLDQNNREHVIDAREPDTV 372
DB 121 LRIYINGDGTGRGTHLSLFFVVMKGNDAIIRWPFNOKVTLMLLDQNNREHVIDAREPDTV 180
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QY 373 TSSSFQRPVNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 422
DB 181 TSSSFQRPVNDMNTASGCLPCPVSKMEAKNSYVRDDAIFKAIVDLTGL 230

RESULT 13
ABU70784
ID ABU70784 standard; protein; 326 AA.
XX AC
XX ABU70784;
XX
XX 10-JUN-2003 (first entry)
XX
XX Human adipocyte Selected Interacting domain, SID, #415.
XX
XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;
XX antidiabetic; protein-protein interaction; diabetes;
XX yeast 2-hybrid assay; metabolic disorder; obesity.
XX
XX Homo sapiens.
XX
XX WO2000286122-A2.
XX
XX PD
XX 31-OCT-2002.
XX
XX 14-MAR-2002; 2002WO-EP003768.
XX
XX 14-MAR-2001; 2001US-0275734P.
XX
XX (HYBR-) HYBRIGENICS.
XX
XX Legrain P, Daviet L;
XX
XX WPI; 2003-103412/09.
XX
XX N-PSDB; ACAS7328.
XX
XX New complex between two interacting proteins in adipocyte cells, useful
XX for identifying selected interacting domains that modulate protein
XX interactions, or for preventing or treating metabolic disorders such as
XX obesity or diabetes.
XX
XX Claim 6; Page 249; 382pp; English.
XX
XX The invention relates to a complex between two interacting proteins in
XX adipocyte cells, given in the specification. The proteins are identified
XX by selecting a bait protein from a known adipocyte marker and then
XX performing a yeast 2-hybrid selection to isolate prey proteins encoded by
XX members of an adipocyte cDNA library. The proteins are designated SID
XX (RTM) (selected interacting domains) proteins. Also included are a
XX polynucleotide encoding a polypeptide in the adipocyte cells, a
XX recombinant host cell expressing at least one of the interacting
XX polypeptides of the complex, selecting a modulating compound in adipocyte
XX cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
XX sequences given in the specification (including its fragment or variant),
XX a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
XX given in the specification (including its fragment or variant), a vector
XX comprising the SID (RTM) polynucleotide, a recombinant host cell
XX comprising the vector, a protein chip comprising the polypeptides and a
XX record comprising all or part of the data, listed in the specification.
XX The complex, polypeptides, polynucleotides and compounds are useful for
XX preventing or treating metabolic disorders such as obesity or diabetes.
XX The polynucleotides are useful as probes or primers. The complex is
XX particularly useful for identifying selected interacting domains (SID
XX (RTM)) for screening drugs that modulate the protein interaction, thus
XX exhibiting the therapeutic effect. The present sequence represents a SID
XX (prey) protein of the invention
XX
XX Sequence 326 AA;
```

Query Match 45.2%; Score 999.5; DB 6; Length 326;
Best Local Similarity 67.8%; Pred. No. 7.6e-89;
Matches 219; Conservative 13; Mismatches 48; Indels 43; Gaps 7;

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; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA: 08/331394
; APPLICATION NUMBER: 08/331394
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ganger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-446-915-4

Query Match      86.6%; Score 1914.5; DB 1; Length 501;
Best Local Similarity 74.3%; Pred. No. 6.4e-184;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAAASVTPGSLLELQPGSKLLGTLEAKYLCSACRNVLRRPFAQCQGHRYCSFCLAS 60
DB 1 MAAASVTPGSLLELQPGSKLLGTLEAKYLCSACRNVLRRPFAQCQGHRYCSFCLAS 60
QY 61 ILSSGPONCAACVHEGYIEGSILESSAFPDNAARREVESLPVCPDGTGCTWKGLKE 120
DB 61 ILSSGPONCAACVHEGYIEGSILESSAFPDNAARREVESLPVCPDGTGCTWKGLKE 120
QY 121 YE----- 122
DB 121 YESCHEGLCPFLITECPACKGLVRLSEKHEHTEQECPKESLSQCHRAPCSHVDLEHVE 180
QY 123 -----FQDHVKTGCKRVPCEPFAIGCLETVGEKQOEHEVOWL 161
DB 181 VCPKPLTCDGCGKKIPRETQDQHVACSKRVLCRFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCVLNREVERVAVTA 221
DB 241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCVLNREVERVAVTA 221
QY 241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCVLNREVERVAVTA 300
DB 241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCVLNREVERVAVTA 300
QY 222 EACSRQHRLDQDKTEALSSKVQQLERSIGLKLAMADLEOKVLEMEASTYDGVFIWKISD 281
DB 301 EACSRQHRLDQDKTEALSSKVQQLERSIGLKLAMADLEOKVLEMEASTYDGVFIWKISD 360
QY 282 FARKLOEAVAGRIPAFISPAFYTSRYGYKMLRIYNGDGTGRGTHLSLFFVVMKGPND 341
DB 361 FARKLOEAVAGRIPAFISPAFYTSRYGYKMLRIYNGDGTGRGTHLSLFFVVMKGPND 420
QY 342 LLRWPNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNITASGCLFPCPVSKMEA 401
DB 421 LLRWPNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNITASGCLFPCPVSKMEA 480
QY 402 KNSYVRDDAIFIKAIVDLTGL 422
DB 481 KNSYVRDDAIFIKAIVDLTGL 501

RESULT 4
US-08-744-139-4
; Sequence 4, Application US/08744139
; Patent No. 5863612
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
```

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; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,139
; FILING DATE: 31-Oct-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 05/27/1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ganger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-744-139-4

Query Match      86.6%; Score 1914.5; DB 2; Length 501;
Best Local Similarity 74.3%; Pred. No. 6.4e-184;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAAASVTPGSLLELQPGSKLLGTLEAKYLCSACRNVLRRPFAQCQGHRYCSFCLAS 60
DB 1 MAAASVTPGSLLELQPGSKLLGTLEAKYLCSACRNVLRRPFAQCQGHRYCSFCLAS 60
QY 61 ILSSGPONCAACVHEGYIEGSILESSAFPDNAARREVESLPVCPDGTGCTWKGLKE 120
DB 61 ILSSGPONCAACVHEGYIEGSILESSAFPDNAARREVESLPVCPDGTGCTWKGLKE 120
QY 121 YE----- 122
DB 121 YESCHEGLCPFLITECPACKGLVRLSEKHEHTEQECPKESLSQCHRAPCSHVDLEHVE 180
QY 123 -----FQDHVKTGCKRVPCEPFAIGCLETVGEKQOEHEVOWL 161
DB 181 VCPKPLTCDGCGKKIPRETQDQHVACSKRVLCRFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCVLNREVERVAVTA 221
DB 241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCSELEKKTATFENIVCVLNREVERVAVTA 300
QY 222 EACSRQHRLDQDKTEALSSKVQQLERSIGLKLAMADLEOKVLEMEASTYDGVFIWKISD 281
DB 301 EACSRQHRLDQDKTEALSSKVQQLERSIGLKLAMADLEOKVLEMEASTYDGVFIWKISD 360
QY 282 FARKLOEAVAGRIPAFISPAFYTSRYGYKMLRIYNGDGTGRGTHLSLFFVVMKGPND 341
DB 361 FARKLOEAVAGRIPAFISPAFYTSRYGYKMLRIYNGDGTGRGTHLSLFFVVMKGPND 420
QY 342 LLRWPNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNITASGCLFPCPVSKMEA 401
DB 421 LLRWPNQKVTMLLDQNNREHVIDAFRDPDVTSSSFQRPVDMNITASGCLFPCPVSKMEA 480
QY 402 KNSYVRDDAIFIKAIVDLTGL 422
DB 481 KNSYVRDDAIFIKAIVDLTGL 501

RESULT 5
US-08-779-599-4
```

Sequence 4, Application US/08779599

Patent No. 6500922

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

APPLICANT: Rothe, Mike

TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/779,599

FILING DATE: 07-Jan-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P0897C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 501 amino acids

TYPE: Amino acid

TOPOLOGY: Linear

US-08-779-599-4

Query Match

Best Local Similarity 86.6%; Score 1914.5; DB 4; Length 501;

Mismatches 74.3%; Pred. No. 6.4e-184;

Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACNVLRPFPQACGHRVCSFCLAS 60

DB 1 MAASVTPSGSLELLQPGFSKTLTGKLEAKYLCACNVLRPFPQACGHRVCSFCLTS 60

QY 61 ILSSGPQNCACVVEGLYEEGISELESSAPPDNAARREVESLPVPCPDGCTWKGTLKE 120

DB 61 ILSSGPQNCACVVEGLYEEGISELESSAPPDNAARREVESLPVPCPDGCTWKGTLKE 120

QY 121 YE----- 122

DB 121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTEQCPKRSLSQCHRAPCSHVLDLVHYE 180

QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVEGEKQOEHEVQWL 161

DB 181 VCPFPFLTDCGCKKIPRETQFQDHVRACSKRVLCRFHTVGCSEWVETENLDHQLRL 240

QY 162 REHLAMLLSSVLEAKPLGQDSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221

DB 241 REHLALLSSFLEAQASPGTLNQVGPPELLQRCQILEQKIATFENIVCVLNREVERVAMTA 300

QY 222 EACSRQRLDQDKLEALSKVQQLERSIGLKDAMADLEQKLEMEASTYDGVFIKISD 281

DB 301 EACSRQRLDQDKLEALSKVQQLERSIGLKDAMADLEQKLEMEASTYDGVFIKISD 360

QY 282 FARKLQEAAGRIIPAIFSPAFYTSRYGYKCLRIYLNQDGTGRGTHLSLFFVVMKGPDA 341

DB 361 FTRKRQEAAGRTIPAIFSPAFYTSRYGYKCLRIYLNQDGTGRGTHLSLFFVVMKGPDA 420

QY 342 LLRPFRQKVTMLLDQNNREHVIDARPDVTSSSFQPVNDMNIASGCLFPCVSKMEA 401

DB 421 LLQWPFQKVTMLLDHNNREHVIDARPDVTSSSFQPVNDMNIASGCLFPCVSKMEA 480

QY 402 KNSYVRDDAIFIKAIIVDLTGL 422

DB 481 KNSYVRDDAIFIKAIIVDLTGL 501

RESULT 6

PCT-US95-06639-4

Sequence 4, Application PC/TUS9506639

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06639

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/250858

FILING DATE: 27-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/331394

FILING DATE: 28-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: 897P2PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 501 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US95-06639-4

Query Match 86.6%; Score 1914.5; DB 5; Length 501;

Best Local Similarity 74.3%; Pred. No. 6.4e-184;

Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACNVLRPFPQACGHRVCSFCLAS 60

DB 1 MAASVTPSGSLELLQPGFSKTLTGKLEAKYLCACNVLRPFPQACGHRVCSFCLTS 60

QY 61 ILSSGPQNCACVVEGLYEEGISELESSAPPDNAARREVESLPVPCPDGCTWKGTLKE 120

DB 61 ILSSGPQNCACVVEGLYEEGISELESSAPPDNAARREVESLPVPCPDGCTWKGTLKE 120

QY 121 YE----- 122

DB 121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTEQCPKRSLSQCHRAPCSHVLDLVHYE 180

QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVEGEKQOEHEVQWL 161

DB 181 VCPFPFLTDCGCKKIPRETQFQDHVRACSKRVLCRFHTVGCSEWVETENLDHQLRL 240

QY 162 REHLAMLLSSVLEAKPLGQDSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221

DB 241 REHLALLSSFLEAQASPGTLNQVGPPELLQRCQILEQKIATFENIVCVLNREVERVAMTA 300

QY 222 EACSRQHRDQDKIEALSSKVOQLERSIGLKDLAVADLEOKVLEMEASTYDGVFIWKISD 281
DB 301 EACSRQHRDQDKIEALSSKVOQLERSIGLKDLAVADLEOKVLEMEASTYDGVFIWKISD 360
QY 282 FARKLQEA VAGRIPAFISPAFTSRYGYKWCRLRIYVNGDGTGRGTHLSLFFVVMKGPND 341
DB 361 FTRKQEA VAGRIPAFISPAFTSRYGYKWCRLRIYVNGDGTGRGTHLSLFFVVMKGPND 420
QY 342 LIRWPNQKVTMLLDONNREHVIDAFRDPVTSSSFQRPVNDMNITASGCLPCPVSKMEA 401
DB 421 LIQWPNQKVTMLLDONNREHVIDAFRDPVTSSSFQRPVNDMNITASGCLPCPVSKMEA 480
QY 402 KNSYVRDDAIFIKAIVDLTGL 422
DB 481 KNSYVRDDAIFIKAIVDLTGL 501

RESULT 7

US-09-181-958-1
; Sequence 1, Application US/09181958
; Patent No. 6143507
; GENERAL INFORMATION:
; APPLICANT: Kehry, Marilyn R
; APPLICANT: Puller, Steven S
; TITLE OF INVENTION: High Throughput Compatible Assays for Receptor-TRAF
; FILE REFERENCE: 9 142 Nucl. Seq
; CURRENT APPLICATION NUMBER: US/09/181,958
; CURRENT FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 243
; TYPE: PRT
; ORGANISM: human
US-09-181-958-1

Query Match 53.3%; Score 1178; DB 3; Length 243;
Best Local Similarity 99.6%; Pred. No. 3.1e-110;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CESLEKKTATFENIVCVLNREVERVAMTAACSRQHRDQDKIEALSSKVOQLERSIGLK 252
DB 1 CESLEKKTATFENIVCVLNREVERVAMTAACSRQHRDQDKIEALSSKVOQLERSIGLK 60
QY 253 DLAMADLEOKVLEMEASTYDGVFIWKISDFARKLQEA VAGRIPAFISPAFTSRYGYKMC 312
DB 61 DLAMADLEOKVLEMEASTYDGVFIWKISDFARKLQEA VAGRIPAFISPAFTSRYGYKMC 120
QY 313 LRIYVNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDPV 372
DB 121 LRIYVNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDPV 180
QY 373 TSSSFQRPVNDMNITASGCLPCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 422
DB 181 TSSSFQRPVNDMNITASGCLPCPVSKMEAKNSYVRDDAIFIKAIVDLTGL 230

RESULT 8

US-08-331-394-2
; Sequence 2, Application US/08331394
; Patent No. 5670319
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,394
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-331-394-2

Query Match 32.9%; Score 727; DB 1; Length 409;
Best Local Similarity 38.5%; Pred. No. 1.8e-64;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;

QY 85 LESSSAFPDAAAREVESLPAVCPSDG-----CTWKGTLEKEVEPDQHVKTGKCR----- 134
DB 1 MASSAPDENEFPQGPCPAPCQDPSEPRVLCCT--ACLSNLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRFAIGCLETVEGEKQOEHEVQMLREHLAMLSSVLE 174
DB 59 VSPGSLPTQEKVHSDVAEABIMCPFFAGVGCGSKGSPQSMQEHATSQSSHLVLLAVLKE 118
QY 175 AKPLGQCSHAGSELLOR-----CES----- 195
DB 119 WKSPGSLNLSAPWALERNLSELQAAVEATGDLVDCYRAPCCESQEBELQHLVKEK 176
QY 196 ----LEKKTATFENIVCVLNREVERVAMTAACSRQHRDQDKIEALSSKVOQLERSIGL 251
DB 179 LLAQLEKLRVANIIVAVLNKEVEASHLAASIHQSQLDREHLLSLEQRVVLELQOTLAQ 238
QY 252 KDLAMADLEOKVLEMEASTYDGVFIWKISDFARKLQEA VAGRIPAFISPAFTSRYGYKM 311
DB 239 KDQVLGKLEHSLRLMEEA SFDGTLWKITNVTKRCHESVCGRTVSLFSPAFYTAKYGYKL 298
QY 312 CLRIYVNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDP 371
DB 299 CLRIYVNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDONNREHVIDAFRDP 358
QY 372 VTSSSFQRPVNDMNITASGCLPCPVSKMEA-KNSYVRDDAIFIKAIYVD 418
DB 359 LSSASFQRPQSETNVASGCLPFLFPLSKLQSPKHYAVKDDTMFLKCIYD 406

RESULT 9

US-08-250-858-2
; Sequence 2, Application US/08250858
; Patent No. 5708142
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 62

RESULT 11
US-08-744-139-2
; Sequence 2, Application US/08744139
; Patent No. 5869612
; GENERAL INFORMATION:
; APPLICANT: Goedel, David V
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,139
; FILING DATE: 31-Oct-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 05/27/1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-744-139-2

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Query Match      32.9%; Score 727; DB 2; Length 409;
Best Local Similarity 38.5%; Pred.No 1.8e-64;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;

QY      85 LESSAPPDNAAREVBSLPAVCPSDG-----CTWKGTILKEYEFQDHVKTCCKR----- 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MASSAPDENEFGCPAPQCDSEPRVLCT--ACLSENLRDDEDRICPKCSADNLHP 58
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      135 -----VPCRFHAIGCLTVEGSKQBEHYQWLREHLAMLLSSVLE 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      59 VSPGSPITQKVHSDVAEAEIMCFAGVGCSPQSPQMQBEHATSSSHYILLAVLKE 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      175 AKPLLGPQSHAGSELLQR-----CES----- 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      119 WKSPGSGNLGSPAWALERNLSLQLQAAVEATGDLVDCYRAPCCESEELALQHLVKEK 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      196 ----LEKKTATFENIVCVLNEVERVAMTABACSRQHRLLDOOKTEALSCKVQQLERSIGL 251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      179 LLAQLESKRLRVANIVAVLNEVEASHLAAASHQSOLDREHLLSLSEQRVVEIQQTLAQ 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      252 KDLAMADLEQVLMEASSTYDGVFTWKISDFARKLQEAVAGRIIPAISPAFVTSRYGYKM 311
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      239 KDQVLGKLEHSLRLMEEFASFGDTFLWKLTNTVKCHESVCQRTVSLFSPAFYTKIYKYL 298
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      312 CLRILYNGDGTGRGTHLSLFPWMKGPNDALLRFPFNQKVTMLMLLDQNNRHSHVIDAFRPD 371
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      299 CLRILYNGDGGKTHLSLFLVIVRGEVDALLPFPFRKNVTFLMLDQNNRHSHVIDAFRPD 358
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      372 VTSSSFQRPVNDMNIAAGCPLFCPVSXMEAE-KNSYVRDDAIFIKAIVD 418
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

359 LSASAFQPSQSTNVASGCPLEFFPLSKQSPKSHAVVKDDTFLKXIVD 400

RESULT 12

US-08-779-599-2

Sequence 2, Application US/08779599

Patent No. 6500922

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

APPLICANT: Rothe, Mike

TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Minipat (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/779,599

FILING DATE: 07-Jan-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Drager, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P0897C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 409 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-779-599-2

Query Match	32.9%;	Score	727;	DB	4;	Length	409;
Best Local Similarity	38.5%;	Pred. No.	1.8e-64;				
Matches	157;	Conservative	63;	Mismatches	112;	Indels	76;
Gaps							
Qy	85	LESSAPDNDNAAREVESLPAVCPSDG----	CTWKGTLKSEYFODHVKTGCKR-----	134			
Db	1	MASSAPDENEFQGCPPACQDPSEPRVLCCT--	ACLSENLRDDEDRICPKCRADNLHP	58			
Qy	135	-----VPCRPHAIGLETVEGEKQOEHEVQWREHLAMLLSSVLE	174				
Db	59	VSPGSPITQEKVHSDVAEAEIMCPFAGVCGSPGSPQSMQEHATSQSSHLVLLAVLKE	118				
Qy	175	AKPLGDOOSHAGSELLQR-----	CEG-----	195			
Db	119	WKSPGSGNLGSAPMALERNLSELQLOAAVEATGDLVDCYRAPCCSEQSEELALQHLVKEK	178				
Qy	196	-----LEKKTATFENIVCVINREVERVANTAEACSRQHRLOODKTEALSSKVQQLERSIGL	251				
Db	179	LLAQLEEKLRVFANIVALNKEVEASHALAAASTHQSLDRHLLSLDEQRVVELQQTIAQ	238				
Qy	252	KDLAMADLEQKLEMEASTVDGVFIWKISDFARKLOEAVAGRIPAIESPAPFYTRYGYKM	311				
Db	239	KQVILGKLEHSLRLMEEASPDGTFELWITVNTKRECHESVCGRTVSLFSPAPFYTRYGYKL	298				
Qy	312	CLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRPFNQKVTLMLLDQNNREHVIDAFRPD	371				
Db	299	CLRIYLNGDSGKKTHLSLFIVIMRGEYDALLPWPFNKVTFMLLDQNNREHVIDAFRPD	358				
Qy	372	VTSSSFQRPVNDMMNIAGCPILFCPVSXWEA-KNSYVRDDAIFIKAIYD	418				

Db 359 LSSASFQRPQSETNVASGCLFFPLSLKQSPKHAHVVDKDTWFLKCIVD 406

RESULT 13
PCT-US95-06639-2
; Sequence 2, Application PC/TUS9506639
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06639
; FILING DATE:
; CLASSIFICATION:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331394
; FILING DATE: 28-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-06639-2

Query Match 32.9%; Score 727; DB 5; Length 409;
Best Local Similarity 38.5%; Pred. No. 1.8e-64;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;
QY 85 LESSAFPDNAARVESLPVAFCSGDG----CTWKGLTKEVEFQDVKTCGKCR----- 134
Db 1 MASSAPDENEFQCCPAPQDSESRVLCCT--ACLSNLRDDDEDRICPKCADNLHP 58
QY 135 -----VPCRFHAIGLTETVEGKQOEHEVQVLRHMLLSVLE 174
Db 59 VSPGSLTQEKVHSDVAEAEIMCPFAGVGCSPQSMQGEHATSQSHYLLAVLKE 118
QY 175 AKPLLGQSHAGSELLOR-----CES----- 195
Db 119 WKSPGSGNLSGAPNALERNISELOQAVENTGDEVDVCPACCSQBELAQLHLVKEK 178
QY 196 ----LEKKTATFENIVCVLNREVERVAMTACSRQHLRDLDOOKIEALSSKVOQLERSIGL 251
Db 179 LLAQLEEKLRVFANIVAVLNKEVEASHALAAASHQSLDREHLLSLEQRWELQOTLAQ 238
QY 252 KDLAVADLEQVLEWAEASTVDGVFIWKISDFARKLOEAVAGRIPAFSPAFYTSRYCYKM 311
Db 239 KDQVGLKLESLRMEASDGTFLWKITNTVKRCHESVCGRTVSFSPAFYATKYGYKL 298
QY 312 CLRILYNGDGTGRGTHLSLFFVVMKGPNDALLRPFNFQKVTLLMLLDQNNREHVIDAFRPD 371

Db 299 CLRILYNGDGSCKTHLSLFIIVIMGEYDALLPWFRNKVTFMLLDQNNREHVIDAFRPD 358

QY 372 VTSSSFQRPVNDMNIIASGCLFPCPVSKMEA-KNSYVRDDAIFKAIVD 418
Db 359 LSSASFQRPQSETNVASGCLFFPLSLKQSPKHAHVVDKDTWFLKCIVD 406

RESULT 14
US-08-697-610-2
; Sequence 2, Application US/08697610
; Patent No. 6172187
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: CD40 Associated Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,610
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,357
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-697-610-2

Query Match 32.4%; Score 717; DB 3; Length 543;
Best Local Similarity 34.9%; Pred. No. 2.9e-63;
Matches 184; Conservative 76; Mismatches 125; Indels 142; Gaps 23;
QY 16 QGPFKTLTGKLEKYLCSACRVLRPPFOAQOCHRYCSCFLASILLSSGPNCAACVHE 75
Db 36 QGQYKEKVT-VEQYKCKCHLVLCSPKQTECHRCSCSCMAALLSSSPKCTAC-QE 93
QY 76 GYBERGIGILSSSAPPDNAARVESLPVAVC--PSDGCTWKGLT----- 118
Db 94 SIVKDKV-----FKDNCCKREILALQIYCRNESRGCAEQTLGHLLVHLKNDCHFE 145
QY 119 -----KE-----YEFODHYK-----TCGKCR--VP-----CRFHAJCC- 144
Db 146 LFCVAPDCKEKVLKDLRDHVKACKYREATCSCKSQVPMIALQKHEDTDCPCVVVSCP 205
QY 145 ---LETV---EGEKQO--BEHVQWLRHMLAML--LSSVLEAKPLLGDQSHAGSELLQRC 193
Db 206 HKCSVQTLRSEGTNQIQAHEASAVQHVNLKENSLEKK-----VSLIQN- 254
QY 194 ESLEKKTAT--TFENIVCVLNREVER-----VAMTAEACS----- 225
Db 255 ESVEKNKSIQSLHNLQICFETIEERQKEMLRNNEKSLILHQRVIDSOAEKLEKDKBIRS 314

Query Match	32.4%;	Score	71.7;	DB	3;	Length	543;	
Best Local Similarity	34.9%;	Pred. No.	2.9e-63;					
Matches 184;	Conservative	76;	Mismatches	125;	Indels	142;	Gaps	23;
Qy	16	QPQFSKTLGTLEAKYLCSCARNVLRPFQAGCHRYCSFCLASILSSGPNQCAACVHE	75					
Db	36	QGYGKZFVKT-VDKYKCEKCHLVLCSPKQTECHRSCESCMAILLSSSPKCTAC-QE	93					
Qy	76	GIYEEGISILESSAPPDNNAREVESIPAVC--PSDGTWKGYL-----	118					
Db	94	SIVKDV-----FKDNCKREITAIQIYCNESRGCARQLTGLHLVHLKNDCHFEE	145					
Qy	119	-----KE--VEFQDHVK-----TGKCR--VP-----CRFHAIGC-	144					
Db	146	LPCVRPDCKEKVLKDLRHDVFKAQYREATCSHCKSOVPMIALQGHEDTDPCVWVSCP	205					

Search completed: November 10, 2004, 16:29:44
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: November 10, 2004, 16:28:24 ; Search time 143 Seconds

(without alignments)
1042.387 Million cell updates/sec

Title: US-10-018-030b-2

Perfect score: 2211

Sequence: 1 MAASVTPPGSLELLQPGFS.....NSVYRDDAIFKAIVDLTGL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata1/pubpaa/CT_NEW_PUB.pep:*
- 3: /cgn2_6/prodata1/pubpaa/US05_NEW_PUB.pep:*
- 4: /cgn2_6/prodata1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/prodata1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/prodata1/pubpaa/CTUS_PUBCOMB.pep:*
- 7: /cgn2_6/prodata1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/prodata1/pubpaa/US09A_PUBCOMB.pep:*
- 9: /cgn2_6/prodata1/pubpaa/US09B_PUBCOMB.pep:*
- 10: /cgn2_6/prodata1/pubpaa/US09C_PUBCOMB.pep:*
- 11: /cgn2_6/prodata1/pubpaa/US09_NEW_PUB.pep:*
- 12: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
- 13: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
- 14: /cgn2_6/prodata1/pubpaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/prodata1/pubpaa/US10D_PUBCOMB.pep:*
- 16: /cgn2_6/prodata1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/prodata1/pubpaa/US11_NEW_PUB.pep:*
- 18: /cgn2_6/prodata1/pubpaa/US60_NEW_PUB.pep:*
- 19: /cgn2_6/prodata1/pubpaa/US60_PUBCOMB.pep:*
- 20: /cgn2_6/prodata1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2047.5	92.6	501	15	US-10-361-270-1
2	1914.5	86.6	501	14	US-10-283-500-4
3	1831.5	73.8	477	14	US-10-094-749-1702
4	730	33.0	586	8	US-08-813-323A-1
5	727	32.9	409	14	US-10-283-500-2
6	722	32.7	543	14	US-10-004-378A-35
7	717.5	32.5	568	8	US-08-813-323A-2
8	717.5	32.5	568	14	US-10-116-275-173
9	717.5	32.5	568	14	US-10-004-378A-36
10	717	32.4	543	9	US-09-757-041-2
11	713.5	32.3	568	15	US-10-042-865-166
12	710	32.1	567	14	US-10-242-212-7
13	710	32.1	567	14	US-10-207-655-103

14	687.5	31.1	538	15	US-10-042-865-163	Sequence 163, App
15	687.5	31.1	557	14	US-10-004-378A-34	Sequence 34, Appl
16	687.5	31.1	557	15	US-10-042-865-162	Sequence 162, App
17	686	31.0	568	15	US-10-262-445-132	Sequence 132, App
18	686	31.0	568	15	US-10-042-865-38	Sequence 38, Appl
19	679.5	30.7	438	9	US-09-950-902-2	Sequence 2, Appli
20	674.5	30.5	417	14	US-10-453-478-18	Sequence 18, Appl
21	664.5	30.1	451	14	US-10-004-378A-2	Sequence 2, Appli
22	664	30.0	526	15	US-10-262-445-130	Sequence 130, App
23	664	30.0	526	15	US-10-042-865-50	Sequence 50, Appl
24	664	30.0	558	14	US-10-004-378A-32	Sequence 32, Appl
25	664	30.0	558	15	US-10-042-865-164	Sequence 164, App
26	659	29.8	558	14	US-10-004-378A-33	Sequence 33, Appl
27	659	29.8	558	15	US-10-042-865-165	Sequence 165, App
28	638	28.9	347	9	US-09-950-902-4	Sequence 4, Appli
29	621	28.7	386	14	US-10-004-378A-4	Sequence 4, Appli
30	457.5	20.1	143	14	US-10-004-378A-38	Sequence 38, Appl
31	424	19.2	530	15	US-10-042-865-131	Sequence 131, App
32	410	18.5	522	15	US-10-042-865-129	Sequence 129, App
33	408	18.5	522	15	US-10-042-865-130	Sequence 130, App
34	378	17.1	526	15	US-10-042-865-24	Sequence 24, Appl
35	255	11.5	131	15	US-10-131-487A-61	Sequence 61, Appl
36	249.5	11.3	72	9	US-09-864-761-33993	Sequence 33993, A
37	206	9.3	43	9	US-09-798-789-3	Sequence 3, Appli
38	206	9.3	43	9	US-09-981-389-3	Sequence 3, Appli
39	206	9.3	43	14	US-10-262-630-25	Sequence 25, Appl
40	198	9.0	399	15	US-10-042-865-132	Sequence 132, App
41	165.5	7.5	61	9	US-09-796-692-857	Sequence 857, App
42	185.5	7.5	61	14	US-10-040-862-857	Sequence 857, App
43	185.5	7.5	61	15	US-10-057-475B-857	Sequence 857, App
44	185.5	7.5	61	15	US-10-154-884B-857	Sequence 857, App
45	165.5	7.5	61	16	US-10-764-324-857	Sequence 857, App

ALIGNMENTS

RESULT 1
US-10-361-270-1
; Sequence 1, Application US/10361270
; Publication No. US20040038299A1
; GENERAL INFORMATION:
; APPLICANT: Kuai, Jun
; APPLICANT: Wocters, Joseph L
; APPLICANT: Nickbarg, Elliott
; APPLICANT: Qiu, Yongchang
; APPLICANT: Lin, Lih-Ling
; TITLE OF INVENTION: Composition and Method for Modulating an Inflammatory
; TITLE OF INVENTION: Response
; FILE REFERENCE: 22058-565
; CURRENT APPLICATION NUMBER: US/10/361,270
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/355,183
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-270-1

Query Match 92.6%; Score 2047.5; DB 15; Length 501;
Best Local Similarity 80.4%; Pred. No. 7e-173;
Matches 403; Conservative 4; Mismatches 15; Indels 79; Gaps 1;

QY 1 MAASVTPPGSLELLQPGFSKTLTGTLKLEAKYLCACRNVLRRPFOACGCHRYCSFCLAS 60
Db 1 MAASVTPPGSLELLQPGFSKTLTGTLKLEAKYLCACRNVLRRPFOACGCHRYCSFCLAS 60

QY 61 ILSSGPQNCACVHEGYIEGISESSAPPDNAAREVESLPAVCPSDCTWKGLTKE 120
Db 61 ILSSGPQNCACVHEGYIEGISESSAPPDNAAREVESLPAVCPSDCTWKGLTKE 120

```

121 YE-----122
121 YESCHGRCPLMLTECPACKGLVRLGKERHLEHECPERSLSCHRCRAPCGADVKAHHE 180
123 -----FQDHVTKGCRVPCRFHAIGCLTVEGEKQHEVQWL 161
181 VCPKPLTCDGCKKKIPREXFDQHVTKGCRVPCRFHAIGCLTVEGEKQHEVQWL 240
162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
222 EACSRQHLDDQDKIEALSSKVQQLERSIGLKDAMADLEQKVLEMEASTYDGVFIWKISD 281
301 EACSRQHLDDQDKIEALSSKVQQLERSIGLKDAMADLEQKVLEMEASTYDGVFIWKISD 360
282 FARKLOEAVAGRIPAIFSPAFYTSRYGYMCLRIYVNGDGTGRGTHLSLFFVVMKGNDA 341
361 ILRLQEAAGRIPAIFSPAFYTSRYGYMCLRIYVNGDGTGRGTHLSLFFVVMKGNDA 420
342 LLRWPFNKVTLMLDDQNNREHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 401
421 LLRWPFNKVTLMLDDQNNREHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 480
402 KNSYVRDDAIFKAIVDTGL 422
481 KNSYVRDDAIFKAIVDTGL 501

RESULT 2
US-10-283-500-4
; Sequence 4, Application US/10283500
; Publication No. US20030120043A1
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,500
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,599
; FILING DATE: 07-Jan-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P0897C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-283-500-4

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Query Match 86.6%; Score 1914.5; DB 14; Length 501;
Best Local Similarity 74.3%; Pred. No. 4.5e-161;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPPGSLELLQPGFSTLLGTLEAKYLCACRNVLRRPFAOCHRYCSFCLAS 60
DB 1 MAASVTPPGSLELLQPGFSTLLGTLEAKYLCACRNVLRRPFAOCHRYCSFCLAS 60
QY 61 ILSSGPQCAACVHEGIYEEGSIILESSAPDPNARREVESLPVCFSDGCTWGTTLKE 120
DB 61 ILSSGPQCAACVHEGIYEEGSIILESSAPDPNARREVESLPVCFSDGCTWGTTLKE 120
QY 121 YE-----122
DB 121 YESCHGRCPLMLTECPACKGLVRLGKERHLEHECPERSLSCHRCRAPCGADVKAHHE 180
QY 123 -----FQDHVTKGCRVPCRFHAIGCLTVEGEKQHEVQWL 161
DB 181 VCPKPLTCDGCKKKIPREXFDQHVTKGCRVPCRFHAIGCLTVEGEKQHEVQWL 240
QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 221
DB 241 REHLAMLLSSVLEAKPLLDQSHAGSELLQRCESLEKKTATFENIVCVLNREVERVAMTA 300
QY 222 EACSRQHLDDQDKIEALSSKVQQLERSIGLKDAMADLEQKVLEMEASTYDGVFIWKISD 281
DB 301 EACSRQHLDDQDKIEALSSKVQQLERSIGLKDAMADLEQKVLEMEASTYDGVFIWKISD 360
QY 282 FARKLOEAVAGRIPAIFSPAFYTSRYGYMCLRIYVNGDGTGRGTHLSLFFVVMKGNDA 341
DB 361 FTRKQEAAGRIPAIFSPAFYTSRYGYMCLRIYVNGDGTGRGTHLSLFFVVMKGNDA 420
QY 342 LLRWPFNKVTLMLDDQNNREHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 401
DB 421 LLRWPFNKVTLMLDDQNNREHVIDAFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 480
QY 402 KNSYVRDDAIFKAIVDTGL 422
DB 481 KNSYVRDDAIFKAIVDTGL 501

RESULT 3
US-10-094-749-1702
; Sequence 1702, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAWATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14

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; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1702
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1702

Query Match
Best Local Similarity 73.8%; Score 1631.5; DB 14; Length 447;
Matches 340; Conservative 17; Mismatches 50; Indels 55; Gaps 9;

QY 1 MAASVTPPGSLELLPGFSGKTLTGKLEAKYLCSACRNVLRRPFOAQCGHYCSFCLAS 60
DB 1 MAASVTPPGSLELLPGFSGKTLTGKLEAKYLCSACRNVLRRPFOAQCGHYCSFCLAS 60
QY 61 ILSSGPNCAACVHGIYEGISILESSAFPDNAARREVESELPVCPDGGCTWGTGLKE 120
DB 61 ILSSGPNCAACVHGIYEGISILESSAFPDNAARREVESELPVCPDGGCTWGTGLKE 120
QY 121 YEFQDHVKTG-----KCRVPCRTHAI-----GLETVEGEKQEHVQWL 161
DB 121 YEFK--MPACGMWTEAPVAGSRSPSSVDLVHPLTGAECALNSVEETE----- 170
QY 162 REHMLLSVLEAK-PL-----LGD-QSHAGSELLORCESLEKKTATFENI 206
DB 171 -----LLRSCHGRCPLMLTECPACKGLVLRGEKERHLEHECPERSLSCHRCRAPCCGA 225
QY 207 VCVLNEV-ERVAMTAACS-----RQRLDQDKIEALSKVOOLERSIGLKLAMADLE 260
DB 226 DVKAHEVCPKPTCDGGCKKIPREKFDQDKIEALSKVOOLERSIGLKLAMADLE 285
QY 261 QKLEMEASTYDGVFIWKISDFARKLQEAAGRIIPAFSPAPYTSRYGKMCIRIYVNGD 320
DB 286 QKLEMEASTYDGVFIWKISDFARKLQEAAGRIIPAFSPAPYTSRYGKMCIRIYVNGD 345
QY 321 GTGRGTHLSLFFVVMKGPNDALLRWPENOKVTLMMLDQNNREHVIDAFPRDVTSSSFQRP 380
DB 346 GTGRGTHLSLFFVVMKGPNDALLRWPENOKVTLMMLDQNNREHVIDAFPRDVTSSSFQRP 405
QY 381 VNDMNIASGCLFCFVSKMEAKNSYVRDDAIFKAIYVDTLGL 422
DB 406 VNDMNIASGCLFCFVSKMEAKNSYVRDDAIFKAIYVDTLGL 447

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RESULT 4
US-08-813-323A-1
; Sequence 1, Application US/08813323A
; Publication No. US20020031522A1
; GENERAL INFORMATION:
; APPLICANT: Baltimore, David
; APPLICANT: Cheng, Genhong
; APPLICANT: Cleary, Aileen
; APPLICANT: Lederman, Seth
; APPLICANT: Ye, Zheng-sheng
; TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,323A
; FILING DATE:
; CLASSIFICATION: 530

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 566 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..566
US-08-813-323A-1

Query Match
Best Local Similarity 33.0%; Score 730; DB 8; Length 566;
Matches 187; Conservative 80; Mismatches 111; Indels 184; Gaps 22;

QY 1 MAASVTPPGSLELLPGFSGKTLTGKLEAKYLCSACRNVLRRPFOA 47
DB 7 MDAAGTLQPNPLKQPDGAGSVLPVPEQGGYKEKFKVT-VEKYGCEKRLVLCNPKQT 65
QY 48 QCGHYCSFCLASILSSGPNCAACVHGIYEGISILESSAFPDNAARREVESELPVAVC 107
DB 66 ECGHRCFSCMAALLSSSSPKCTAC-QESIHKDV-----FKDNCCREIALLQVYC 116
QY 108 PSD--GCTWGTGL-----KEYEQ-----DHVK-----TC 130
DB 117 RNEGRGCAEQTLGHLVHLKNEQCFEELPCLRADCKEKLRLKDLRDHVEKACKYREATC 176
QY 131 GKCR--VP-----CRFAI 142
DB 177 SHKSVQPMIKLQKHEDTDCPVVSCPHKCSVQTLRSELSELSAHLSECVNAPSTCSFRRY 236
QY 143 GCLETVEGEKQ--EHEVQWLRLEHML--LSSVLEAKPLLGDSHAGSELLQRCESLEK 198
DB 237 GCV--FQGTNQIKAHEASSAVQHVNLKWSNSLEK-----VSLQN-ESVEK 283
QY 199 KTA--TFENIVCVLNREVER-----VAMTAACS-----RQHR 229
DB 284 NKISQLHNOICSPFEIERQKEMLRNNEKILHQLRVIDSQAEKLEKDEIRPFRRQNW 343
QY 230 LDQD----KIEALSKVOOLE-----RSIGLKDLAMADLEQ 261
DB 344 EADSMSKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLNVHDIRLADMDL 403
QY 262 KYLEMEASTYDGVFIWKISDFARKLQEAAGRIIPAFSPAPYTSRYGKMCIRIYVNGDG 321
DB 404 RFQVLETAASVNGVLIWKIRYKRRKQEAVMGKTLISYSQPPFYTGFGYKMCARYVNGDG 463
QY 322 TGRGTHLSLFFVVMKGPNDALLRWPENOKVTLMMLDQ--NNREHVIDAFPRDVTSSSFQRP 380
DB 464 MKGTHLSLFFVIMRGEVDALLPWFQKQVTLMMLDQSSRRHLGDAFKPDPSNSSFQKP 523
QY 381 VNDMNIASGCLFCFVSKMEAKNSYVRDDAIFKAIYVDTLGL 422
DB 524 TGMNIASGCPVFVAQTVLE-NGTVIKDDTIFIKVIVDTSDL 564

RESULT 5
US-10-283-500-2
; Sequence 2, Application US/10283500
; Publication No. US20030120043A1
; GENERAL INFORMATION:
; APPLICANT: Goettel, David V.
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 59

```

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/283,500
 ; FILING DATE: 30-Oct-2002
 ; CLASSIFICATION: <Unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/779,599
 ; FILING DATE: 07-Jan-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: P0897C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-3216
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ;
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 409 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ;
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-283-500-2

Query Match 32.9%; Score 727; DB 14; Length 409;
 Best Local Similarity 38.5%; Pred. No. 1e-55;
 Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;
 QY 85 LESSAFPDNAARREVESLPVCSGSDG---CTWKGLTKEYEFODHVKTCKGCE-----134
 DB 1 MASSSAPDENEFQFCPPAPQDFSEPRVLCT--ACLSNLRDDEDRICPKCRADNLHP 58
 QY 135 -----VPCRHAIGCLETVEGEKQOEHEVQWLRHLAMLSSVLE 174
 DB 59 VSPGSLTQEKVHSDVAEABIMCPFAGVGCSPQSMQHEATSSSHLYLLAVLKE 118
 QY 175 AKPLIGDQSHAGSELLQR-----CES-----195
 DB 119 WKSPFGSLGAPWALERNLSLQLOAAVEATGDLVDVCPACCSQEBELALQHLVKEK 178
 QY 196 ----LEKTAFTENIVCVLNREVERVAMTACRQRHRLDQDKTEALSSKVVQLERISGL 251
 DB 179 LLAQLEELRVANIVAVLNKEVEASHALAAASHQSLDREHLLSLQEVVELQQTQA 238
 QY 252 KDLAMADLEQKLEWASTYGVFWKISDFARKLQEAQVAGRIPAIFSPAFYTSRYGYKM 311
 DB 239 KDQVGLKLESLRLMEBASFGTLFWKITNTVKCHESVCGRTVSLSPAFYAKYGYKL 298
 QY 312 CLRILYNGDGTGRGTHLSLFFVVMKGNDAALLRPFNQKVTMLLDQNNREHVDAFRPD 371
 DB 299 CLRILYNGDGSKKTHLSLFLVIMRGEYDALLPWFNFKVTFTMLDQNNREHAIDAFRPD 358
 QY 372 VTSSSFQRPVNDMNTASCPFLFCPVSKWEA-KNSYVRRDDAIFIKAIYD 418
 DB 359 LSSASFQRPQSETNVASCCPLFFFLSLQSPKHAIVKDDTNFLKCIYD 406

RESULT 6
 US-10-004-378A-35
 ; Sequence 35, Application US/10004378A
 ; Publication No. US20030228301A1
 ; GENERAL INFORMATION:

; APPLICANT: Li, Li
 ; APPLICANT: Furtak, Kazaryna
 ; APPLICANT: Perna, Amanda
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Guo, Xiaojia Sasha
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Malyanekar, Uriel M
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Vernet, Corinne A
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Agee, Michele
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shenoy, Suresh G
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Alsbrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Edinger, Schlomit
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Peyman, John A
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Stone, David J
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Gangolli, Esha A
 ; TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding The
 ; TITLE OF INVENTION: Methods of Using the Same
 ; FILE REFERENCE: 21402-179
 ; CURRENT APPLICATION NUMBER: US/10/004,378A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,892
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,765
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/300,206
 ; PRIOR FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: 60/242,789
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,768
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/242,767
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: 60/243,622
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: 60/273,047
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: 60/243,591
 ; PRIOR FILING DATE: 2000-10-26
 ; PRIOR APPLICATION NUMBER: 60/243,950
 ; PRIOR FILING DATE: 2000-10-27
 ; Remaining prior application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 191
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 35
 ; LENGTH: 543
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-004-378A-35

Query Match 32.7%; Score 722; DB 14; Length 543;
 Best Local Similarity 34.9%; Pred. No. 4.1e-55;
 Matches 184; Conservative 77; Mismatches 124; Indels 142; Gaps 23;
 QY 16 QGFGSKTLGTGLKLEAKYLCASCRNVLRPPFOAQCHRYCSCCLASILLSSGPNCAACVHE 75
 DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRCFCECMALJSSSSPKCTAC-QE 93
 QY 76 GIYEGISILESSSAFPDAAARREVESLPVAVC--PSDQCTWKGLT-----118
 DB 94 SIVKDKV-----FKDNCCKREILALQIYCRNESRCAEQTLTLHLVHLKNDCHPEE 145
 QY 119 -----KE-----YEFQDHVK-----TCGKCR---VP-----CRFHAIGC- 144

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Db 146 LPCRDPCKEVLRLDRHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205
QY 145 ---LTV---EGEKQ--EHEVQWLRHLAML--LSSVLEAKPLIGDQSHAGSELLQRC 193
Db 206 HKCSVQTLRSEGTNOQIKAHHEASSAVQHVNLKKEWSNLEKK-----VSLQV- 254
QY 194 ESLEKTA--TFENIVCVLNREVER-----VAMTAEACS----- 225
Db 255 ESVEKNKSIQSLHNOICSPFEIETEROKEMLRNESKILHLQRLVIDSOAEKLELDEKIRS 314
QY 226 -RQRLDQD---KIEALSKVQOLE-----RSIGL-----XDLAM 256
Db 315 FRQWBEADSMKSSVESLQNRVTELESVDKSAQVARNLTGLESQSLRHDQMLSVHDIRL 374
QY 257 ADLEQVLEMEASTYDGVFTWIKISDFARKIQAVAGRIAPAFSPFYTSRYGYKMCRLRY 316
Db 375 ADMDLRFQVLETSYNGVLIWKIRYKRRKQEAIVGKTSLSYQPFYTGFGYKMCARY 434
QY 317 LNDGTRGTHLSLFFVVMKGNPDALLRWPFPKQVTLMLLDQ--NNREHVIDAFRDPVTSS 375
Db 435 LNDGNGKGTHTLSLFFVIMRGEYDALLPWPFPKQVTLMLMDQSSRRHLGDAFKDPNNS 494
QY 376 SFORPVNDMNIASGCLFPCVSKMEAKNSVYRDDAIFIKAIVDLTGL 422
Db 495 SFKKPTGEMNIASGCPVFVAQTVLE--NGTYIKDDTIFIKVIVDTSGL 540

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RESULT 7

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US-08-813-323A-2
; Sequence 2, Application US/0813323A
; Publication No. US20020031522A1
; GENERAL INFORMATION:
; APPLICANT: Baltimore, David
; APPLICANT: Cheng, Genhong
; APPLICANT: Cleary, Aileen
; APPLICANT: Lederman, Seth
; APPLICANT: Ye, Zheng-sheng
; TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham, LLP
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/813,323A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50659
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..568

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US-08-813-323A-2
Query Match
Best Local Similarity 32.5%; Score 717.5; DB 8; Length 568;
Matches 184; Conservative 75; Mismatches 124; Indels 171; Gaps 22;
QY 16 QPGFSKTLTGKLEAKYLCACRNVLRRPFAQCGHRYCSFCLASILSSSPQNCACVHE 75
Db 36 QGGYKEXFVKT--VEDKYKCEKCHLVLCSPKQTEGCHRFCEBSCMAALSSSPKCTAC--QE 93
QY 76 GIVEEGSILSSSAFPDAAARREVESLPAVC--PSDGTWKGTL----- 118
Db 94 SIVKDKV-----FDNCKREILALQIYCRNESGCAEQLTLGHLVLKNDCHFE 145
QY 119 -----KE---YEFQDHVK-----TCGKCR--VP----- 136
Db 146 LPCVRPDCKEKVLRLDRHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCP 205
QY 137 -----CRFHAIGLETVEGEKQ--EHEVQWLRHLAML 168
Db 206 HKCSVQTLRSELSAHLSECVNAPSTCSFKRYGCV--FQTNQOIKAHEASSAVQHVNL 263
QY 169 --LSSVLEAKPLIGDQSHAGSELLQRCSELEKTA--TFENIVCVLNREVER----- 216
Db 264 KEWSNLEKK-----VSLQV--ESVEKNKSIQSLHNOICSPFEIETEROKEMLRN 312
QY 217 -----VAMTAEACS-----RQRLDQD---KIEALSKVQOLE----- 246
Db 313 ESKILHLQRLVIDSOAEKLEKDEIRPFRQWBEADSMKSSVESLQNRVTELESVDKSA 372
QY 247 ---RSIGL-----XDLAMADLEQVLEMEASTYDGVFTWIKISDFARKIQEA 289
Db 373 QVARNLTGLESQSLRHDQMLSVHDIRLADMDLRQVLETSYNGVLIWKIRYKRRKQEA 432
QY 290 VAGRIPAIFSPFYTSRYGYKMCRLRYIYNGDGTGRTGTHLSLFFVVMKGNPDALLRWPFP 349
Db 433 VMGKTSLSYQPFYTGFGYKMCARVYNGDMGKGTHTLSLFFVIMRGEYDALLPWPFPKQ 492
QY 350 KVTLMMLDQ--NNREHVIDAFRDPVTSSSFORPVNDMNIASGCLFPCVSKMEAKNSVYRD 408
Db 493 KVTLMMLDQSSRRHLGDAFKDPNNSSFKPTGEMNIASGCPVFVAQTVLE--NGTYIKD 551
QY 409 DAIFIKAIVDLTGL 422
Db 552 DTIFIKVIVDTSGL 565

```

RESULT 8

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US-10-116-275-173
; Sequence 173, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 173
; LENGTH: 568
; TYPE: PRI
; ORGANISM: Homo sapiens
US-10-116-275-173

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Query Match
Best Local Similarity 32.5%; Score 717.5; DB 14; Length 568;
33.2%; Pred. No. 1.1e-54;

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Matches 184; Conservative 75; Mismatches 124; Indels 171; Gaps 22;
QY 16 QGFSKTLTGKLEAKYLCACRNVLRRPFOAQOCHRYCSFCLASILLSSGPNCAACVHE 75
Db 36 QGYKEKPVKT-VEKYKCEKCHLVLCSPKQTECHRFCECMAALLSSSPKCTAC-QE 93
QY 76 GYIEGSILESSAPPNAAARVESLPAVC--PSDGTWKGTL----- 118
Db 94 SIVKQV-----FKDNCCKREILALQIYCRNESGCAEQTLGLHLLVHLKNDCHFEE 145
QY 119 -----KE--YEFQDHVK-----TCGKCR--VP----- 136
Db 146 LPCVRPDCKEKVLKDLRDHVEKACKYREATCSHCQSQVPMIALQKHEDTDCPCVVVSCP 205
QY 137 -----CRFHAIGCLETVEGEKQO--EHEVQWLREHLAML 168
Db 206 HKCSVQTLRLSELSEHSAHSECVNAPSTCSFKRYGCV--FQGTNQIQAHEASSAVQHVNL 263
QY 169 --LSSVLEAKPLLGQSHAGSELLQRCSELEKTA--TFENIVCVLNEVER----- 216
Db 264 KEWSNSLEKK-----VSLQN-ESVEKNKSIQSLHNQICSPFEIERQKEMLRNN 312
QY 217 -----VAMTAEACS-----RQRLDQD-----KIEALSSKVOOLE----- 246
Db 313 ESKILHLQVIDSQAEKLEKLDKEIRPPRQNWESADSMKSSVESLQNRVTELESVDKXAG 372
QY 247 ---RSIGL-----KDLAMADLEQKLEVEASTYDGVFIWKISDFARKLQEA 289
Db 373 QVARTGLESQSLSRHDQMSVHDIRLADMDLRVQLVETASYNGLVWKIRYKRRQEA 432
QY 290 VAGRIPAIFSPAFYTSRYGKMCRLIYNGDGTGRGTHLSLFFVVMKGPNDALLRWPFO 349
Db 433 VMGKTLISYQPFYTGFGYKMCARVYNGDMGKGTLSLFFVIMRGEVDALLPWFQK 492
QY 350 KVTMLLDQ--NNREHVIDAFRPDVTSSSFQRPVNDMNIAACPLFCFVSKMEAKNSYVRD 408
Db 493 KVTMLMDQSSRRHLGDAFDPDNSSSFKPTGEMNIAACPLFCFVSKMEAKNSYVRD 551
QY 409 DAIFKAIVDLTGL 422
Db 552 DTIFKIVIDTSDL 565

RESULT 9
US-10-004-378A-36
; Sequence 36, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Furtak, Kazarzyna
; APPLICANT: Perna, Amanda
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard A
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Casman, Stacie J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Vernet, Corrine A
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Agee, Michele
; APPLICANT: Rastelli, Luca
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Grosse, William M
; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Gerlach, Valerie
; APPLICANT: Edinger, Schlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Peyman, John A
; APPLICANT: Gunther, Erik
; APPLICANT: Store, David J
; APPLICANT: Ellerman, Karen

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; APPLICANT: Gangolli, Esha A
; TITLE OF INVENTION: No. US20030228301A1el Human Proteins, Polynucleotides Encoding The
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 21402-179
; CURRENT APPLICATION NUMBER: US/10/004,378A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/242,882
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,765
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/300,206
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/242,789
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,768
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,767
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/243,622
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/273,047
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/243,591
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,950
; PRIOR FILING DATE: 2000-10-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-004-378A-36

Query Match 32.5%; Score 717.5; DB 14; Length 568;
Best Local Similarity 33.2%; Pred. No. 1.1e-54;
Matches 184; Conservative 75; Mismatches 124; Indels 171; Gaps 22;

QY 16 QGFSKTLTGKLEAKYLCACRNVLRRPFOAQOCHRYCSFCLASILLSSGPNCAACVHE 75
Db 36 QGYKEKPVKT-VEKYKCEKCHLVLCSPKQTECHRFCECMAALLSSSPKCTAC-QE 93
QY 76 GYIEGSILESSAPPNAAARVESLPAVC--PSDGTWKGTL----- 118
Db 94 SIVKQV-----FKDNCCKREILALQIYCRNESGCAEQTLGLHLLVHLKNDCHFEE 145
QY 119 -----KE--YEFQDHVK-----TCGKCR--VP----- 136
Db 146 LPCVRPDCKEKVLKDLRDHVEKACKYREATCSHCQSQVPMIALQKHEDTDCPCVVVSCP 205
QY 137 -----CRFHAIGCLETVEGEKQO--EHEVQWLREHLAML 168
Db 206 HKCSVQTLRLSELSEHSAHSECVNAPSTCSFKRYGCV--FQGTNQIQAHEASSAVQHVNL 263
QY 169 --LSSVLEAKPLLGQSHAGSELLQRCSELEKTA--TFENIVCVLNEVER----- 216
Db 264 KEWSNSLEKK-----VSLQN-ESVEKNKSIQSLHNQICSPFEIERQKEMLRNN 312
QY 217 -----VAMTAEACS-----RQRLDQD-----KIEALSSKVOOLE----- 246
Db 313 ESKILHLQVIDSQAEKLEKLDKEIRPPRQNWESADSMKSSVESLQNRVTELESVDKXAG 372
QY 247 ---RSIGL-----KDLAMADLEQKLEVEASTYDGVFIWKISDFARKLQEA 289
Db 373 QVARTGLESQSLSRHDQMSVHDIRLADMDLRVQLVETASYNGLVWKIRYKRRQEA 432
QY 290 VAGRIPAIFSPAFYTSRYGKMCRLIYNGDGTGRGTHLSLFFVVMKGPNDALLRWPFO 349
Db 433 VMGKTLISYQPFYTGFGYKMCARVYNGDMGKGTLSLFFVIMRGEVDALLPWFQK 492
QY 350 KVTMLLDQ--NNREHVIDAFRPDVTSSSFQRPVNDMNIAACPLFCFVSKMEAKNSYVRD 408

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Db 493 KVTMLMDQSGRRHLGDAFKDPDNNSSPKPTGEMNIASGCPVFAQTIVLE-NGTYIKD 551
QY 409 DAIFIKAIYDLTGL 422
Db 552 DIIFIKVIVDTSDL 565

RESULT 10
US-09-757-041-2
; Sequence 2, Application US/09757041
; Patent No. US20020009726A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: CD40 Associated Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/757,041
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/349,357
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-757-041-2

Query Match 32.4%; Score 717; DB 9; Length 543;
Best Local Similarity 34.9%; Pred. No. 1.1e-54;
Matches 184; Conservative 76; Mismatches 125; Indels 142; Gaps 23;

QY 16 QPGFSKLLGTKLEAKYLSACRNVLRRPFOAQCGHYCSFCLASTLSSGPNQACVHE 75
Db 36 QGSGYKEKFKVT-VEDRYKCEKCHLVCSFKQTECGHRSCESCMAALLSSSPKCTAC-QE 93
QY 76 GIYEEGISILESSAFPDMARVESLPVC--PSDGCTWGTLL----- 118
Db 94 SIYKDKV-----FKDNCCKREILALQYCRNESRGCAEQTLGLHLVLKNDCHFE 145
QY 119 -----KE---YFQDHVK-----TCGKCR--VP-----CRFHAIGC- 144
Db 146 LPCRVDCKEVLKRLDRHVEKACKYREATCSHCKSQVPMALQKHEDTDCFCVVVSCP 205
QY 145 -----LETV-----EGEKQO---EHEVQMLREHLAML--LSSVLEAKPLIGDQSHAGSILLQRC 193
Db 206 HKCSVQTLRLSEGTNOQIKAHASSAVQVNLKWSNSLEKK-----VSLQK- 254
QY 194 ESLEKXTA--TFENIVCVLNREVER-----VAMTARACS----- 225
Db 255 ESVEKNKIQSLNQNICSFEIERQKEMLRNNEKILHLQRLVIDSQAEKLEKLEKRS 314

QY 226 -RQHRLDQD----KIEALSSKVOOLE-----RSIGL-----KDLAM 256
Db 315 FRQWEEADSMKSSVESLQNRVTELESVDKSAQVARNVTGLLESQLSRHPQMLSVHDRL 374
QY 257 ADLEQKVLNEASTYDQVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSYGYKXCLRIY 316
Db 375 ADMDLRFQVLETASVNGVLIWKIRDYKRRKQEAVMGKTLISLYSQFFYTGFGYKMCARVY 434
QY 317 LNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNOKVTLMMLDQ--NNREHVIDAFRPDVTSS 375
Db 435 LNGDMGKGTHTLSLFFVIMRGEVDALLPWFPKQKVTLMMDQSGRRHLGDAFKDPDSS 494
QY 376 SFQRPVNDMNIASGCPFCFSVKMEAKNSVYRDDAIFIKAIVDLTGL 422
Db 495 SFKKPTGEMNIASGCPVFAQTIVLE-NGTYIKDDTIPIKIVIVDTSDL 540

RESULT 11
US-10-042-865-166
; Sequence 166, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Serence L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 166
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-042-865-166

Query Match 32.3%; Score 713.5; DB 15; Length 568;
Best Local Similarity 32.7%; Pred. No. 2.5e-54;
Matches 181; Conservative 75; Mismatches 127; Indels 171; Gaps 21;

QY 16 QGFSKTLTGKLEAKYLCSACRNVLRRPFOACQCHRYCSFCLASILSSGPONCAACVHE 75
DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRFCSMAALLSSSPKCTAC-QE 93
QY 76 GIYEGISILESSAFPPDAAARREVESLPAVC--PSDGT-----113
DB 94 SIVKDKV-----FKDNCCKREILALQIYCRNESRGCAEQMLGLHLVHLKNDCHFEEL 145
QY 114 -----WKGTLKEYEFQDHVK-----TCGKCR--VP-----136
DB 146 PCVRPDCKEKVLKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDPCVVVSCP 205
QY 137 -----CRFHAIGCLETVGEKQO--EHEVQWLREHLAML 168
DB 206 HKCSVQTLRLSELSELSAHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAEASAVQHVNL 263
QY 169 --LSSVLEAKPLLDGSHAGSELLQRCESLEKTA--TFENIVCVLNREVER-----216
DB 264 KEWNSLEKK-----VSLIQN-ESVEKNKSIOQLHNOICSEFEIERQKEMLRNN 312
QY 217 -----VAMTAACCS-----RQRLDQD-----KIEALSSKVOOLE-----246
DB 313 ESKILHQRVIDSQAEKLEKELDKIRPPRQNWEEADSMKSVESLQNRVTELSVDKSG 372
QY 247 ---RSIGL-----KDLAVADLEQKVLMEASTYDGVFIWKISDFARKLQEA 289
DB 373 QVARNTGLLESQSRHDQMSVHDIRLADMDLRFQVLETASYNGVLKIRDYKRRKQEA 432
QY 290 VAGRIPAFSPAYTSRYGYKMCRLIYNGDGTGRGTHLSLFFVVMGPNDAALLRPFPNQ 349
DB 433 VMGKTLISYQFFYTGFGYKMCARVYNGDGMKGTHLSLFFVIMRGYDALLPWPFKQ 492
QY 350 KVTMLMDQ--NNREHVIDAFPRDPTSSSFQPVNDMNIAAGCPLFCFVSKMEAKNSYVRD 408
DB 493 KVTMLMDQSSRRHLGDFAKPDNSSFKPTGEMNIAAGCPLFCFVVAQTGLE-NGYIKD 551
QY 409 DAIFIKAIVDLTGL 422
DB 552 DTIFKIVIDTSDL 565

RESULT 12

US-10-242-212-7
; Sequence 7, Application US/10242212
; Publication No. US2003009644A1
; GENERAL INFORMATION:
; APPLICANT: AHUJA, SEEMA
; APPLICANT: BONEWALD, LYNDIA
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 4003.001000
; CURRENT APPLICATION NUMBER: US/10/242.212
; PRIOR FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-212-7

Query Match 32.1%; Score 710; DB 14; Length 567;
Best Local Similarity 32.7%; Pred. No. 5.1e-54;
Matches 181; Conservative 74; Mismatches 128; Indels 170; Gaps 21;

QY 16 QGFSKTLTGKLEAKYLCSACRNVLRRPFOACQCHRYCSFCLASILSSGPONCAACVHE 75
DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRFCSMAALLSSSPKCTAC-QE 93
QY 76 GIYEGISILESSAFPPDAAARREVESLPAVC--PSDGT-----113
DB 94 SIVKDKV-----FKDNCCKREILALQIYCRNESRGCAEQMLGLHLVHLKNDCHFEEL 145
QY 114 -----WKGTLKEYEFQDHVK-----TCGKCR--VP-----136
DB 146 PCVRPDCKEKVLKDLRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDPCVVVSCP 205
QY 137 -----CRFHAIGCLETVGEKQO--EHEVQWLREHLAML- 168
DB 206 KCSVQTLRLSELSELSAHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAEASAVQHVNL 263
QY 169 --LSSVLEAKPLLDGSHAGSELLQRCESLEKTA--TFENIVCVLNREVER-----216
DB 264 EWSNSLEKK-----VSLIQN-ESVEKNKSIOQLHNOICSEFEIERQKEMLRNN 312
QY 217 -----VAMTAACCS-----RQRLDQD-----KIEALSSKVOOLE-----246
DB 313 SKILHQRVIDSQAEKLEKELDKIRPPRQNWEEADSMKSVESLQNRVTELSVDKSG 372
QY 247 ---RSIGL-----KDLAVADLEQKVLMEASTYDGVFIWKISDFARKLQEA 290
DB 373 VARNTGLESQSRHDQMSVHDIRLADMDLRFQVLETASYNGVLKIRDYKRRKQEA 432
QY 291 AGRIPAFSPAYTSRYGYKMCRLIYNGDGTGRGTHLSLFFVVMGPNDAALLRPFPNQ 350
DB 433 MGKTLISYQFFYTGFGYKMCARVYNGDGMKGTHLSLFFVIMRGYDALLPWPFKQ 492
QY 351 VTLMLDQ--NNREHVIDAFPRDPTSSSFQPVNDMNIAAGCPLFCFVSKMEAKNSYVRD 409
DB 493 VTLMLMDQSSRRHLGDFAKPDNSSFKPTGEMNIAAGCPLFCFVVAQTGLE-NGYIKD 551
QY 410 AIFIKAIVDLTGL 422
DB 552 DTIFKIVIDTSDL 564

RESULT 13

US-10-207-655-103
; Sequence 103, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207.655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-103

Query Match 32.1%; Score 710; DB 14; Length 567;
Best Local Similarity 32.7%; Pred. No. 5.1e-54;
Matches 181; Conservative 74; Mismatches 128; Indels 170; Gaps 21;

QY 16 QGFSKTLTGKLEAKYLCSACRNVLRRPFOACQCHRYCSFCLASILSSGPONCAACVHE 75
DB 36 QGGYKEKFKVT-VEKYKCEKCHLVLCSPKQTECHRFCSMAALLSSSPKCTAC-QE 93
QY 76 GIYEGISILESSAFPPDAAARREVESLPAVC--PSDGT-----113
DB 94 SIVKDKV-----FKDNCCKREILALQIYCRNESRGCAEQMLGLHLVHLKNDCHFEEL 145
QY 114 -----WKGTLKEYEFQDHVK-----TCGKCR--VP-----136

Db 146 PCVRPCKEKLKLDLDRHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPH 205
QY 137 -----CRFAIGCLETVEGEKQ--EHEVQWLRHLAML- 168
Db 206 KCSVQILLRSELSEHAHSECVNAPSTCSFKRYGCV--FOGTNOQIKAHAEASSAVQHVNLK 263
QY 169 -LSSVLEAKPLLDQSHAGSELQRCESLEKTA--TFENIVCVLNREVER----- 216
Db 264 EWSNSLEKK-----VSLIQN-ESVEKNKSIQSLHNQICSPFEIERQKEMLRNNE 312
QY 217 -----VAMTAERCS-----RQRLDOD-----KIEALSSKVQOOLE----- 246
Db 313 SKILHLQRLVIDSOAEKLKELDKERIFPRQNWEEADSMKSSVESLQNRVTELESVDKSAQ 372
QY 247 --RSIGL-----KDLAMADLEQKLEMEASTYDGVFTWKISDFARKQEA 290
Db 373 VARTGULSRLSRHPDMSVHDRLADMDLGFQVLETASYNGVLWIKIRDYKRRKQEA 432
QY 291 AGRIPAFSPFTSYRYGYMCLIRIYVNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNOK 350
Db 433 MGKTLSTYSQPFYTGFGYMKCARVYVNGDGMKGTHLSLFFVIMEGEYDALLPWPFOK 492
QY 351 VTLMMLDQ--NRRHVDIAPFPDVTSSSFPYVNDNMNIASGCLFCFVSKWEAKNSYRDD 409
Db 493 VTLMMLDQSSRRHLGDAPDPDNSSFRKPTGEMNIASGCPVFAQTVLIE-NGYIKDD 551
QY 410 AIFIKAIVDLTGL 422
Db 552 TFIKIVDTSD 564

RESULT 14

US-10-042-865-163
; Sequence 163, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangalli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rotherberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: Macdougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09

; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 163
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-163
Query Match 31.1%; Score 687.5; DB 15; Length 538;
Best Local Similarity 30.2%; Pred. No. 4.7e-52;
Matches 160; Conservative 85; Mismatches 139; Indels 145; Gaps 12;
QY 27 KLEAKYLCACRNLYRRPFQAQCGHRYCSCFLASI--LSSGPQNCAACVHEGIEGISI 84
Db 19 RLEERYKCAFCCHSLHNPHTGCGHRFCQHCILSRLNTPV-----ICPVDKEV 68
QY 85 LESSAPPDNAAREVESLPAVCP--SDGCTWKGTGTLKEYEFQDHVYTC-----CKCR 134
Db 69 IKSEVFKDNCCKREVLNLYVYCNAPGCNAKVLGRY--QDHLQOCLFQPVQCSNEKR 126
QY 135 VP-----KATTFENIVCVLNREVERVA----- 136
Db 127 EPVLRKDLKEHLSASCQFRKEKCLYCKDVVWVNLQNHENLCPEYFVFCNNCAKILK 186
QY 137 -----CRFAIGCLETVEGEKQOEHEVQWLRHLAMLSSVLEAKPLLG 180
Db 187 TEVDEHLAVCPAEQDCPFKHYGCAVTDKRNLCQOEHSHALREHMLVLKXNVLQEEQIS 246
QY 181 D----QSHAGSELLQRCESLEK-----KTATFENIVCVLNREVERVA----- 218
Db 247 DLHKSLEQESKIQQLAETIKLEKEPKQPAQLFGKNGSLFNPQVFAHSHIDKSANLEAQ 306
QY 219 ---MTAEACSRQHRLD---QDKIEALSSKVQOOLERS-----IGLKD 254
Db 307 VHQLLMVNVQOQNKFDLRPLMEAVDTVKQKITLLENDDQRLAVLEETNKHDTINIHKA 366
QY 255 AMADLEQKLEMEASTYDGVFIWKISDPARKLOBAVAGRIPAPSPAFYTSRYGYMCLR 314
Db 367 QLSKNEERFKLLEGTCTYNGKLIWKVTDYKMKRRAVDGHTVSIQSFYTSRCGYRJCAR 426
QY 315 IYLMGDTGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDQNNREHVIDAFRPDVT 374
Db 427 AYLVNGDGSGRGSHLSLYFVVMRGEFDSLLQWFPFRQVTLMLDQSGKKNIMETFKPDPS 486
QY 375 SSFQRPVNDNMNIASGCLFCFVSKWE-AKNSYVDDDAIFKAIYDLTGL 422
Db 487 SSFQRPDGMNIASGCPRFVAHSLVLENKAKYIKDDTLFLKVAVDLTDL 535

RESULT 15

US-10-004-378A-34
; Sequence 34, Application US/10004378A
; Publication No. US20030228301A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Furtak, Kazarzyna
; APPLICANT: Perna, Amanda
; APPLICANT: Patturajan, Meera
; APPLICANT: Shmukets, Richard A
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Casman, Stacie J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Vernet, Corrine A

```

; APPLICANT: Spytek, Kimberly A
; APPLICANT: Agee, Michele
; APPLICANT: Rastelli, Luca
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Gerlach, Valerie
; APPLICANT: Edinger, Schlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Peyman, John A
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David J
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A
; TITLE OF INVENTION: No. US2003028301A1el Human Proteins, Polynucleotides Encoding Th
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 21402-179
; CURRENT APPLICATION NUMBER: US/10/004,378A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/242,882
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,765
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/300,206
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/242,789
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,768
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,767
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/243,622
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/273,047
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/243,591
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/243,950
; PRIOR FILING DATE: 2000-10-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 34
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-004-378A-34

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Query Match 31.1%; Score 687.5; DB 14; Length 557;
Best Local Similarity 30.2%; Pred. No. 4.9e-52;
Matches 160; Conservative 85; Mismatches 139; Indels 145; Gaps 12;

QY 27 KLEAKYLCSACRNVLRPFQACGHRVCSFCLAST--LSSGPQNCACVHEGIVEGISI 84
Db 38 RLEERYKCAFCHSVLHNPHQTCGGRPCQHCILSLRELNTVP-----ICPVDKEV 87
QY 85 LESSSAFPDAAARREVSPLAVCP-SDGCTWKGTKEYEFQDHVKTCT-----GKCR 134
Db 88 IKSQEVFNDCKREVLNLYVYCSNAPGCAKAVILGRY--QDHLQCCLPQPVQCSNEKCR 145
QY 135 VP-----136
Db 146 EFLVRKDLKEHLSASCQPKRCKLYCKDKVVVNLQNHENLCEPEYVFCPNNAKILK 205
QY 137 -----CRFHAIGCLETVEGSKQOEHEVQWLRHLAMLSSVLEAKPLLG 180
Db 206 TEVDHLAVCPAEQDCPFKHGCAVTDKRNLOQHEHSALREHMLVLEKNVQLEEQIS 265
QY 181 D-----QSHAGSELQRCBSLEK-----KATPENIVCVLNREVERVA-----218
Db 266 DLHKSLEQKSKIQQLAETIKKLEKFKQPAQLFGKNGSLPNTIQVFASHIDKSAMLEAQ 325

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QY 219 ---MTAEACSRORLID---QDKIEALSSKVOQLERS-----IGLKDL 254
Db 326 VHQLLQMVNQCNKFDLRPLMEAVDTVKQITLLENNQORLAVLEETNKHDTNIIHKA 385
QY 255 AWADLEQKYLEMEASTYDGVFIWKISDFARKLQEAAGRIPAFSPAFVTSRYGYKMCILR 314
Db 386 QLSKNEERFKLLEGTCYNGKLIWKVIDYKMKKREAVDGHVTSIFSQSYTSCGRLCAR 445
QY 315 IYLNQDGTGRTGTHLSLFFVVMKGPNDALLRWPFNQKVTLMMLDQNNREHVIDAFRPDVT 374
Db 446 AYLNQDGTGRTGTHLSLFFVVMKGPNDALLRWPFNQKVTLMMLDQNNREHVIDAFRPDVT 374
QY 375 SSFQRPVNDMNITASGCPLEFCPVSKME-AKNSVYVRDDAIFIKAVDLTGL 422
Db 506 SSFQRPVNDMNITASGCPLEFCPVSKME-AKNSVYVRDDAIFIKAVDLTGL 422

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Search completed: November 10, 2004, 16:40:31
Job time : 147 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2004, 16:19:28 ; Search time 39 Seconds
(without alignments)
1041.115 Million cell updates/sec

Title: US-10-018-030B-2

Perfect score: 2211

Sequence: 1 MAASVTTPGSLLELQPGFS.....NSVVRDAIFKAIYDLTGL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2156.5	97.5	501	2 S56163	tumor necrosis fac
2	1914.5	86.6	501	2 I61912	TNF receptor assoc
3	733.5	33.2	416	2 B55649	TNFR-associated pr
4	730	33.0	567	2 I49272	CD40 receptor-asso
5	727	32.9	409	2 A54750	TNF receptor assoc
6	722	32.7	543	2 S68467	CD40 receptor-asso
7	717.5	32.5	568	2 A55960	tumor necrosis fac
8	687.5	31.1	557	2 JC6539	MLN 62 protein - h
9	496	22.4	470	2 I38026	probable interleuk
10	408	18.5	522	2 S71821	hypothetical prote
11	395	17.9	509	2 T22328	endopeptidase 2 (E
12	139	6.3	748	2 S24334	neprin A (EC 3.4.2
13	135	6.1	704	2 A48040	recombination acti
14	133.5	6.0	1073	2 I51055	neprin A (EC 3.4.2
15	132.5	6.0	668	2 A42908	neprin A (EC 3.4.2
16	131	5.9	746	1 HYHUMA	neprin A (EC 3.4.2
17	124	5.6	760	2 A40195	probable zinc-bind
18	123.5	5.6	624	2 S28418	transcription regu
19	123	5.6	442	2 A57041	ring finger B-box
20	122	5.5	638	2 JC7753	neprin A (EC 3.4.2
21	122	5.5	700	1 HYHUMB	kinesin-related pr
22	121	5.5	2954	2 T14156	RING finger protei
23	119.5	5.4	506	2 S37583	recombination-acti
24	118	5.3	1043	2 B33754	testis-abundant fi
25	115.5	5.2	518	2 JC7387	hypothetical prote
26	115	5.2	944	2 T28734	transforming prote
27	114	5.2	801	4 TVHURE	ret finger protein
28	113.5	5.1	513	1 TVHURF	PML-1 protein - hu
29	113.5	5.1	560	2 A40044	

RESULT 1

S56163

tumor necrosis factor type 2 receptor associated protein - human

N:Alternate names: TNF receptor-associated protein

C:Species: Homo sapiens (man)

C>Date: 10-Oct-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004

C:Accession: S56163; S58925; S58926; I38729

R:Song, H.Y.; Donner, D.B.

Biochem. J. 309, 825-829, 1995

A:Title: Association of a RING finger protein with the cytoplasmic domain of the human t

A:Reference number: S56163; MUID:95366958; PMID:7639698

A:Accession: S56163

A:Molecule type: mRNA

A:Residues: 1-501 <SON1>

A:Cross-references: UNIPROT:Q12933; EMBL:U12597; NID:9975272

R:Song, H.Y.; Donner, D.

submitted to the EMBL Data Library, July 1994

A:Description: Association of a RING finger protein with the cytoplasmic domain of the h

A:Reference number: S58925

A:Accession: S58925

A:Molecule type: mRNA

A:Residues: 1-42,63-342,363-501 <SON2>

A:Cross-references: EMBL:U12597; NID:9975272

A:Accession: S58926

A:Molecule type: mRNA

A:Residues: 1-342,'RPPQACGHRYSFCLASIL',363-501 <SON3>

A:Cross-references: EMBL:U12597; NID:9975272; PIDN:AAAB7706.1; PID:9975273

R:Roche, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.

Cell 78, 681-692, 1994

A:Title: A novel family of putative signal transducers associated with the cytoplasmic do

A:Reference number: A54750; MUID:94349371; PMID:8069916

A:Accession: I38729

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-342,'RPPQACGHRYSFCLASIL',363-501 <ROT>

A:Cross-references: EMBL:U12597; NID:9975272; PIDN:AAAB7706.1; PID:9975273

C:Genetics:

A:Gene: GDB:TRAF2; TRAF

A:Cross-references: GDB:6268629; OMIM:601895

A:Map position: 9q34-q34

C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology

C:Keywords: zinc finger

F:30-78/Domain: RING finger homology <RNG>

Query Match 97.5%; Score 2156.5; DB 2; Length 501;

Best Local Similarity 84.0%; Pred. No. 3.5e-151;

Matches 421; Conservative 0; Mismatches 1; Indels 79; Gaps 1;

OY 1 MAASVTTPGSLLELQPGFSKTLTGKLEAKYLCSACRNVLRRPFOACGHRYSFCLAS 60

DB 1 MAASVTTPGSLLELQPGFSKTLTGKLEAKYLCSACRNVLRRPFOACGHRYSFCLAS 60

QY 61 ILSSGPQCAACVHGIYEEGIISSLESSAFPDNAAREVESLPAVCPSDCTWKGTKE 120
 |||||
 Db 61 ILSSGPQCAACVHGIYEEGIISSLESSAFPDNAAREVESLPAVCPSDCTWKGTKE 120
 |||||
 QY 121 YE----- 122
 ||
 Db 121 YESCHGRCPMLTECPACKGLVRLGEXERHLEHPCPERSLSRCHRAPCCGADVKAHE 180
 ||
 QY 123 ----- 124
 ||
 Db 181 VCPKPLTCDGCKKKIPREFQDHVTCGRVPCRFHAIGCLTVEGEKQHEVQWL 161
 |||||
 QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 221
 |||||
 Db 241 REHLAMLLSSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 300
 |||||
 QY 282 EACSRQHRLDQDKIBALSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 281
 |||||
 Db 301 EACSRQHRLDQDKIBALSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 360
 |||||
 QY 361 FRKLOEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 341
 |||||
 Db 420 FRKLOEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 420
 |||||
 QY 402 KNSYVRDDAIFKAIVDLTGL 422
 |||||
 Db 481 KNSYVRDDAIFKAIVDLTGL 501
 |||||
 RESULT 2
 I61512
 TNFR-associated factor 2 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I61512
 R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
 Cell 78, 681-692, 1994
 A>Title: A novel family of putative signal transducers associated with the cytoplasmic d
 A:Reference number: A54750; MUID:94349371; PMID:8069916
 A:Accession: I61512
 A>Status: preliminary; translated from GS/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-501 <RES>
 A:Cross-references: UNIPROT:P39429; GB:L35303; NID:G532620; PIDN:AAC37662.1; PID:G532621
 C:Genetics:
 A:Gene: TRAF2
 C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C:Keywords: zinc
 F:30-78/Domain: RING finger homology <RNG>
 Query Match 86.6%; Score 1914.5; DB 2; Length 501;
 Best Local Similarity 74.3%; Pred. No. 2.4e-133;
 Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;
 QY 1 MAASVTPPGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRFPQACGHRVCSFCLAS 60
 |||||
 Db 1 MAASVTPSGSLELLQPGFSKTLTGKLEAKYLCACRNVLRRFPQACGHRVCSFCLAS 60
 |||||
 QY 61 ILSSGPQCAACVHGIYEEGIISSLESSAFPDNAAREVESLPAVCPSDCTWKGTKE 120
 |||||
 Db 61 ILSSGPQCAACVHGIYEEGIISSLESSAFPDNAAREVESLPAVCPSDCTWKGTKE 120
 |||||
 QY 121 YE----- 122
 ||
 Db 121 YESCHGLCPPLLTECPACKGLVRLSEKHHTHEQCEPKRSLSQCHRAPCSHVDLVHYE 180
 |||||
 QY 123 ----- 124
 ||
 Db 181 VCPKPLTCDGCKKKIPREFQDHVTCGRVPCRFHAIGCLTVEGEKQHEVQWL 161
 |||||
 Db 181 VCPKPLTCDGCKKKIPREFQDHVTCGRVPCRFHAIGCLTVEGEKQHEVQWL 240
 |||||

QY 162 REHLAMLLSSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 221
 |||||
 Db 241 REHLAMLLSSVLEAKPLLDQSHAGSELLORCESLEKKTATFENIVCVLNREVERVAMTA 300
 |||||
 QY 222 EACSRQHRLDQDKIBALSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 281
 |||||
 Db 301 EACSRQHRLDQDKIBALSKVQOLERSIGLKDLMADLEQKLEMEASTYDGVFIWKISD 360
 |||||
 QY 282 FRKLOEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 341
 |||||
 Db 361 FRKLOEAVAGRIPAIFSPAFYTSRYGKMCRLRYLNGDGTGRGTHLSLFFVVMKGPND 420
 |||||
 QY 342 LLRWPNQKVTMLLDQNNREHVIDAFRDPVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 401
 |||||
 Db 421 LLRWPNQKVTMLLDQNNREHVIDAFRDPVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA 480
 |||||
 QY 402 KNSYVRDDAIFKAIVDLTGL 422
 |||||
 Db 481 KNSYVRDDAIFKAIVDLTGL 501
 |||||
 RESULT 3
 B55649
 TNFR-associated protein EB16 - human
 C:Species: Homo sapiens (man)
 C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C:Accession: B55649
 R:Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.
 Cell 80, 389-399, 1995
 A>Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for
 A:Reference number: A55649; MUID:95163092; PMID:7859281
 A:Accession: B55649
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-416 <MOS>
 A:Cross-references: UNIPROT:Q13077; GB:U19261; NID:9675461; PIDN:AAA62309.1; PID:9675462
 Query Match 33.2%; Score 733.5; DB 2; Length 416;
 Best Local Similarity 37.8%; Pred. No. 1.8e-46;
 Matches 156; Conservative 65; Mismatches 109; Indels 83; Gaps 6;
 QY 55 SFCLASILSSGPQ-----CAACVHGIYEEGIISSLESSAFPDNAAREVESLPAVCPS 109
 |||||
 Db 35 ALCCAGCUSENPRNGEDQICPKRGEDL-----QSISPGSLRTQSKAHEV--- 81
 |||||
 QY 110 DGCTWKGTLEKEYEFDQHVTCGRVPCRFHAIGCLTVEGEKQHEVQWLREHLAMLL 169
 |||||
 Db 82 -----AEAGICGCPFAGVCGSPKSGPSQVQHEVTSQTSHLNLL 120
 |||||
 QY 170 SSVLEAKPLLDQSHAGSELLOR-----CE----- 194
 |||||
 Db 121 GFMKQKARLGCLESGPMALQNLSDLQQAEEVAGDLEVDYCRAPCSQEBELAQH 180
 |||||
 QY 195 -----SLEKKTATFENIVCVLNREVERVAMTAACSRQHRLDQDKIBALSKVQOLE 246
 |||||
 Db 181 FMKELLAELGKLRVFNIVAVLNKEVEASHALATSIHQSLDREILSLEQVVELQ 240
 |||||
 QY 247 RSIGLKDLAMADLEQKLEMEASTYDGVFIWKISDPARKLOEAVAGRIPAIFSPAFYTSR 306
 |||||
 Db 241 QTLAQDQALGKLEQSLRMBEASPDGTFLWKITNVTTRCHESACGRTVSLFSPAFYAK 300
 |||||
 QY 307 YGYKMCRLRYLNGDGTGRGTHLSLFFVVMKGPNDALRWPNQKVTMLLDQNNREHVID 366
 |||||
 Db 301 YGYKMCRLRYLNGDGTGRGTHLSLFFVVMKGPNDALRWPNQKVTMLLDQNNREHVID 360
 |||||
 QY 367 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA-KNSYVRDDAIFKAIVD 418
 |||||
 Db 361 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEA-KNSYVRDDAIFKAIVD 413
 |||||
 RESULT 4
 I49272

CD40 receptor-associated factor 1 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
 C/Accession: I49272
 C/Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
 Science 267, 1494-1498, 1995
 A/Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
 A/Reference number: A55960; MUID:95184010; PMID:7533327
 A/Accession: I49272
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-567 <RES>
 A/Cross-references: UNIPROT:Q60803; EMBL:U21050; NID:g719292; PIDN:AAC52175.1; PID:g719292
 C/Genetics:
 A/Gene: CRAF1
 C/Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C/Keywords: zinc finger
 F/48-96/Domain: RING finger homology <RNG>

Query Match 33.0%; Score 730; DB 2; Length 567;
 Best Local Similarity 32.1%; Pred. No. 4.9e-46;
 Matches 187; Conservative 80; Mismatches 131; Indels 184; Gaps 22;

QY 1 MAAASVTPPGSLLOP-----GFSKTLTGKLEAKYLCACRNVRPFOA 47
 Db 7 MDAAGTLQNPPLKLPDRGAGSVLPVQGGYKEKFKVT-VEKDYKCEKRLVLCNPKQT 65
 QY 48 QCHRRVCSFCLASILSGPQNCACVHGIEYEGISILESSAAPPDPAARREVSIPAVC 107
 Db 66 ECHRRFCESCAALLSSSPKPTAC-QESIIIDKV-----FDNCCRBILALQVYC 116
 QY 108 PSD-GCTWKGTL-----KEYEFGQ-----DHYK-----TC 130
 Db 117 RNSGRCAEQLTGLHLLVHLNCEQFEELPCLRADCKEVLKDLRDHVEKACKYREATC 176
 QY 131 GKCR-VP-----RPFHAI 142
 Db 177 SHCKSQVPMIKLQKHEDTDCPVVSCPHKCSQVTLRLSELSAHLSECVNAPSTCSFKRY 236
 QY 143 GCLTVEGEKQQ--EHEVQWLRHLAML--LSSVLEAKPLGQSHAGSELLQRCSELEK 198
 Db 237 GCV--FGQTQQQIKAEASSAVQVNLKWSNLEKK-----VSLIQN-ESVEK 283
 QY 199 KTA--TFENIVCVLNREVER-----VAMTAEACS-----RQHR 229
 Db 284 NKSIQSLHNOICFETIEIEROKEMLRNNEKILHLQKVIDSOAEKLKELDKIRPRQNW 343
 QY 230 LDQD-----KLEALSSKVOOLE-----RSIGLKOLAMADLEQ 261
 Db 344 EADSMKSSVESLQNRVTELESVDKSAGQARNTGLLESQSHDQTLVSHDIRLADMDL 403
 QY 262 KVLEMEASTYDGVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSRYGYKMLRIYILNGDG 321
 Db 404 RFQVLETASNGVLIWKIRDYKRRKQEAENVGKTLISLYSQPFYTYGYGYKWCARVYLNGDG 463
 QY 322 TGRGTHLSLFPVWKGNDALLRWPQNKVKTMLLDQ--NNREHVIDAFDPDVTSSSFQRP 380
 Db 464 MGKGTHTLSLFPVIMRGEDYDALLPWPFKQKVTMLMDQSGSSRRHLGDAFKPDNSSSFKXP 523
 QY 381 VNDMNIAAGCPFCFVPSKMAKNSYVRDDAIFIKAVDITGL 422
 Db 524 TGMNIAAGCPVFAQTIVLE-NGTYIKDDTIFIKVIVDITGL 564

RESULT 5
 A54750
 TNF receptor associated factor 1 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: A54750
 R/Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
 Cell 78, 661-692, 1994
 A/Title: A novel family of putative signal transducers associated with the cytoplasmic d

A/Reference number: A54750; MUID:94349371; PMID:8059916
 A/Accession: A54750
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-409 <RES>
 A/Cross-references: UNIPROT:P39428; GB:L35302; NID:g532618; PIDN:AAC37663.1; PID:g532619
 C/Genetics:
 A/Gene: TRAF1

Query Match 32.9%; Score 727; DB 2; Length 409;
 Best Local Similarity 38.5%; Pred. No. 5.4e-46;
 Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;

QY 85 LESSAPDPAARREVSLEPAVCSDG-----CTWKGTLKEYEFODHVKTGKCR----- 134
 Db 1 NASSAPDENEFQGCPPAPQDPSEPRVLCCT--ACLSNLRDDEDRICPKCRADNLHP 58
 QY 135 -----VPCRFAIGCLTVEGEKQEQHEVQWLRHLAMLSSVLE 174
 Db 59 VSPGSLTQEKVHSDVAEAEIMCPFAGVGCFSKSPQSMQHEATSSSHLYLLAVLKE 118
 QY 175 AKPLLDGSHAGSELLQR-----CES----- 195
 Db 119 WKSPPGSLGAPALERNLSELOQAQAEATGDLVDVCRAPCCESQEEALQHLVKEK 178
 QY 196 ----LEKKTATFENIVCVLNREVERVAMTAEACSRQHRLDQDKIEALSSKVQQLERSIGL 251
 Db 179 LLAQLEELKRVFANIVAVLNKEVEASHLALAASHQSLDREHLLSLEQRVVELOQTILAQ 238
 QY 252 KDLAMADLEQKVLMEASTYDGVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSRYGYK 311
 Db 239 KDQVLGKLEHSLRLMEBASFDGTFLWKITNTVKRCHESVCGRTVSLFSPAFYTKYGYKL 298
 QY 312 CLRIYLNCDGGRGTHLSLFPVWKGNDALLRWPQNKVKTMLLDQNNRHSHVIDAFRPD 371
 Db 299 CLRIYLNCDGSGKTHLSLFIIVMRGEYDALLPFPFNKVTFFMLDQNNREHVIDAFRPD 358
 QY 372 VTSSSFQRPVNDMNIAAGCPFCFVPSKMAE-KNSYVRDDAIFIKAVD 418
 Db 359 LSSASFQRPQSETNVASGCPFLFFPLSKLQSPKHAYVKDDTMFLKCIVD 406

RESULT 6
 S68467
 CD40 receptor-associated protein CAP-1 - human
 C/Species: Homo sapiens (man)
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: S68467; I53498
 R/Sato, T.; Irie, S.; Reed, J.C.
 FEBS Lett. 358, 113-118, 1995
 A/Title: A novel member of the TRAF family of putative signal transducing proteins binds
 A/Reference number: I53498; MUID:95129692; PMID:7530216
 A/Accession: S68467
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-343 <SAL>
 A/Cross-references: UNIPROT:Q13114; EMBL:L38509; NID:g695357; PIDN:AAA68195.1; PID:g695357
 A/Experimental source: tissue-type fetal brain
 C/Genetics:
 A/Gene: CAP-1
 C/Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 C/Keywords: homodimer; signal transduction; zinc finger
 F/49-97/Domain: RING finger homology <RNG>

Query Match 32.7%; Score 722; DB 2; Length 543;
 Best Local Similarity 34.9%; Pred. No. 1.8e-45;
 Matches 184; Conservative 77; Mismatches 124; Indels 142; Gaps 23;

QY 16 QGFESKTLTGKLEAKYLCACRNVRPFOAQCGHYCSFCLASILSSGQNCACVHE 75
 Db 36 QGGYKEKFKVT-VEKDYKCEKCHLVLCSPKQTEGCHRFCSMAALLSSSPKPTAC-QE 93
 QY 76 GIYERGISILESSAAPPDPAARREVSIPAVC--PSDGCTWKGTL----- 118

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Db 94 SIVKDV-----FKNCCKREILALQIYCRNRSRGCACQTLGLHLLVHLKNDCHFEE 145
QY 119 -----KE-----YEFQDHVK-----TCGKCR--VP-----CRFHAIGC- 144
Db 146 LPCVRPDCCKEVLRLDRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVWSCP 205
QY 145 ----LETV----EKEKQO--EHEVQMLREHLAML--LSSVLEAKPLLGQSHAGSELLQRC 193
Db 206 HKCSVQTLRSEGTNQOIKAHASAVQHVNLKREWSNLEKK-----VSLQN- 254
QY 194 ESELEKKA--TFENIVCVLNREVER-----VAMTAEACS----- 225
Db 255 ESVERKNSIQSLHNOICFSFEIEIERQKEMLRNNSKILHLQVRIDQAEKLEKLDKEIRS 314
QY 226 -RQELDDO---KTEALSSKVOOLE-----RSIGL-----KDLAM 256
Db 315 FRQWEEADSMKSSVESLQNRVTELESVDKSGAGQVARTNGLLESQLSRHDQVLSVHDRL 374
QY 257 ADLEQKVLMEASTYDGVFIWKISDFARKLQEAQVAGRIPAFISPAFYTSRYGYKMCRLIY 316
Db 375 ADMDLRFQVLETASVNGVLIWKIRYKRRKQEAQVNGKTLISYQPFYTGFGYKMCARVY 434
QY 317 LMGCTGRTGTHLSLFFVVMKGNDAALLRPENQKVTMLLDO--NNREHVIDAFEPDVTSS 375
Db 435 LMGDMGRTGTHLSLFFVIMRGEDYDALLPFPKQKVTMLMDQGSRRHLGDAFKPDNNS 494
QY 376 SFQRPVNDMNIASGCPFCPCPKMEAKNSYVRDDAIFIKAIIVDTLGL 422
Db 495 SFPKPTGEMNIASGCPVFVAQTGLE--NGTYIKDDTIFIKIVDTSDL 540

RESULT 7
A:Species: Homo sapiens (man)
N:Alternate names: CD40-binding protein
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C:Accession: A55960; A55135
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
A:Title: Involvement of CRAFI, a relative of TRAF, in CD40 signaling.
A:Reference number: A55960; MUID:95184010; PMID:7533327
A:Accession: A55960
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568 <RES>
A:Cross-references: UNIPROT:Q13114; EMBL:U21092; NID:G726087; PIDN:AA50112.1; PID:G7260
R:Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.
Cell 80, 389-399, 1995
A:Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for
A:Reference number: A55649; MUID:95163092; PMID:7859281
A:Accession: A55649
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-128, 'M', 130-568 <MOS>
A:Cross-references: GB:U19260; NID:G675459; PIDN:AAA65732.1; PID:G675460
R:Hu, H.M.; O'Rourke, K.; Bocurski, M.S.; Dixit, V.M.
J. Biol. Chem. 269, 30069-30072, 1994
A:Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.
A:Reference number: A55135; MUID:95073988; PMID:7527023
A:Accession: A55135
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-128, 'M', 130-133, 135-404, 'G', 406-568 <HUA>
A:Cross-references: GB:U15637; NID:G595910; PIDN:AAA56753.1; PID:G595911
C:Genetics:
A:Gene: CRAFI
C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
C:Keywords: coiled coil; zinc
F:49-97/Domain: RING finger homology <RNG>

Query Match 32.5%; Score 717.5; DB 2; Length 568;

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Best Local Similarity 33.2%; Pred. No. 4.1e-45;
Matches 184; Conservative 75; Mismatches 124; Indels 171; Gaps 22;

QY 16 QPQFSKTLTGKLEAKYLCACRNVLRRPFOACQGHRYCSFCLASILSSGPQNCACVHE 75
Db 36 QGQYKEFKVKT-VEQYKCEKCHLVLCSPKQTECHRRFCESCAAALLSSSPKCTAC-QE 93
QY 76 GIYEEGISELESSAPPDNAARVESLPAVC--PSDGGCTWKGTL----- 118
Db 94 SIVKDV-----FKNCCKREILALQIYCRNRSRGCACQTLGLHLLVHLKNDCHFEE 145
QY 119 -----KE-----YEFQDHVK-----TCGKCR--VP----- 136
Db 146 LPCVRPDCCKEVLRLDRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVWSCP 205
QY 137 -----HKCSVQTLRSELSAHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAHASAVQHVNL 263
Db 206 HKCSVQTLRSELSAHLSECVNAPSTCSFKRYGCV--FOGTNQOIKAHASAVQHVNL 263
QY 169 --LSSVLEAKPLLGQSHAGSELLQRCESLEKKA--TFENIVCVLNREVER----- 216
Db 264 KEWSNLSLEKK-----VSLQN--ESVEKXKSIQSLHNOICFSFEIEIERQKEMLRNN 312
QY 217 -----VAMTAEACS-----RQELDDO---KTEALSSKVOOLE----- 246
Db 313 ESKILHLQVRIDQAEKLEKLDKEIRPFQWEEADSMKSSVESLQNRVTELESVDKSGAG 372
QY 247 ---RSIGL-----KDLAMADLEQKVLMEASTYDGVFIWKISDFARKLQEA 289
Db 373 QVARTNGLLESQLSRHDQVLSVHDRLADMDLRFQVLETASVNGVLIWKIRYKRRKQEA 432
QY 290 VAGRIPAFISPAFYTSRYGYKMCRLIYNGDGTGTHLSLFFVVMKGNDAALLRPENQ 349
Db 433 VMGKTLISYQPFYTGFGYKMCARVYNGDMGKGTHTLSLFFVIMRGEDYDALLPFPKQ 492
QY 350 KVTMLLDO--NNREHVIDAFRPDVTSSGFQRPVNDMNIASGCPFCPCPKMEAKNSYVRD 408
Db 493 KVTMLMDQGSRRHLGDAFKPDNNSFKKPTGEMNIASGCPVFVAQTGLE--NGTYIKD 551
QY 409 DAIFIKAIIVDTLGL 422
Db 552 DTIFIKIVDTSDL 565

RESULT 8
JC6539
tumor necrosis factor receptor-associated factor 5 homolog - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: JC6539
R:Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Yama
Gene 207, 135-140, 1998
A:Title: Cloning and characterization of a cDNA encoding the human homolog of tumor necr
A:Reference number: JC6539; MUID:98172745; PMID:9511754
A:Accession: JC6539
A:Molecule type: mRNA
A:Residues: 1-557 <MIZ>
A:Cross-references: UNIPROT:Q00463; DDBJ:AB000509; NID:G2982670; PIDN:BAA25262.1; PID:G2
C:Comment: This protein is involved in transduction of signals from various tumor necrosi
mpthotoxin-beta receptor.
C:Genetics:
A:Map position: 1q32.3-1q41.1
C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
C:Keywords: coiled coil; tumor; zinc finger
F:41-90/Domain: RING finger homology <RNN>

Query Match 31.1%; Score 687.5; DB 2; Length 557;
Best Local Similarity 30.2%; Pred. No. 6.4e-43;
Matches 160; Conservative 85; Mismatches 139; Indels 145; Gaps 12;

QY 27 KLEAKYLCACRNVLRRPFOACQGHRYCSFCLASI--LSSGPQNCACVHEGIYEGISI 84
Db 38 RLEERYKCAFCHSVLHNPHTGCGHRFCQHCILSRELNTVP-----ICPVDKEV 87

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QY 85 LESSAPPDAAARVESIPAVCP--SDGCTWKTGLKEYFQDHVTKC-----GKCR 134
 Db 88 IKSQEVKDNCKREVNLNLYVYCSNAPGNAKVIILGRY--QDHLQOCLFPQVQCSNEKR 145
 QY 135 VP-----136
 Db 146 EPVLRKDLKEHLSASCQFRKEKCLYCKKDVVNLQNHBEENLCPEYVFCPNNCAKILIK 205
 QY 137 -----CRFHAICGLTVEGEKQOEHEVQWLEHRLHMLSSVLEAKPLIG 180
 Db 206 TEVDEHLAVCEAEQDCPFKHYCAVTDKRNLLQOEHSALREHMLVLEKVNQLEEQIS 265
 QY 181 D-----QSHAGSELLQRCESLEK-----KTATFENIVCVLNEVERVA-----218
 Db 266 DLHKSLEQESKIQOQAEITIKLEKEFKPOAQLFGNGSFLPNIQVFASHIDKSAWLEAQ 325
 QY 219 ---MTAEACSRQRLD---QDXIEALSSKVQQLERS-----TGLKDL 254
 Db 326 VHQLQWVNOQNKFDLRPLMEAVDTVKQITLLENNODORLAVLEBETNKDTHINIKHA 385
 QY 255 AMADLEQKLEMEASTYDGVFIKISDPARKLOEAVAGRIPAIFSPAFYTSRYGYKMCILR 314
 Db 386 QLSKNEERFKLLEGTGKNGKLIWKVTDYKMKKEAVDGTSTVFSQSFTSRGYNLCAR 445
 QY 315 IYINGDGTGRGTHLSLFFVVMKGPNDALLRWPNQKVTMLMLDQNNREHVIDAFRDPVTS 374
 Db 446 AYINGDGSGRGSHLSLYFVVMRGEFDSLLQWPRQRVQVTMLMLDQSKNIMETFKEDPNS 505
 QY 375 SSFQRPVNDMNIAAGCPFLCPVSKME-AKNSYVRDDAIFIKAIIVDTLGL 422
 Db 506 SSFQRPDGMNIAAGCPFRVAHSLVLENAKNAYIKDPTFLKVAVDLTL 554
 RESULT 9
 I38026
 MLN 62 protein - human
 C:Species: Homo sapiens (man)
 C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 07-Jul-2003
 C:Accession: I38026; S60681
 R:Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.
 Genomics 28, 367-376, 1995
 A>Title: Identification of four novel human genes amplified and overexpressed in breast
 A:Reference number: I37080; MUID:96039245; PMID:7490069
 A:Accession: I38026
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-470 <RES>
 A:Cross-references: EMBL:X80200; NID:951276; PIDN:CAA56491.1; PID:951277
 A>Note: submitted to the EMBL Data Library, July 1994
 C:Gene: CART1
 C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 F;14-63/Domain: RING finger homology <RRN>
 Query Match 22.4%; Score 496; DB 2; Length 470;
 Best Local Similarity 28.5%; Pred. No. 6.6e-29;
 Matches 147; Conservative 62; Mismatches 142; Indels 164; Gaps 21;
 QY 17 PGFSKTLGLKBAKYLCSACRNVRPFPQ-AQCGRHYCSFCLASILSSGPNQCAACVHE 75
 Db 2 PGDYLKL-EKPRRLJLCPICGKPMREPQVSTCGHRFCDTCLQEFLESEGVFK-----54
 QY 76 GIVEGSIILESSAPPDNAAREVSLPAVC--PSDGGCTWKTGLKEYFQDHVTKC--131
 Db 55 ---PEDQLPLDYAKIYDPDPELVQVLGRLPRTCHSHSEGRWSGFLR--HLQGLHNTCSFN 109
 QY 132 -----KCRVPCRFHAIGCLETVEGEKQOEHEVQWLEHRL 165
 Db 110 VFCPNRCPKLSEKRLPAHLQHDQCPKRLKCFE--CGC--DFSGAYSHSEGMCPQESV 165
 QY 166 -----AMLLSSVLEAKPLIGQSHAGSELLQ-----CESL 196

Db 166 YCENKCGARNMRGLL-----AQHATSECPKETQCTYCTKEFVFDTIQSHOYQCPL 217
 QY 197 E-----KKTATFENIVC-----VLNREVE-----R 216
 Db 218 PVACPNQCGVGTAREDLPGHLKDCSNTALVLCFPFGCKGCKHRCFKLAMARHVEESVKPH 277
 QY 217 VAMTAACSRQRLDQDKIEALSCKVQQLERSIGLKOLAMADLEQKLEMEASTYDGVFI 276
 Db 278 LAMCALVSRQ-----ELQELRRE--LEELS VGS-----DGVLI 311
 QY 277 WKISDFARKLOEAVAGRIPAIFSPAFYTSRYGYKMCILRIYNGDGTGRGTHLSLFFVVMK 336
 Db 312 WKIGSYGRRLQEAQAKNLECFSPAFYTHKYGYKQVSAFLNGSGEGTHLSLYIRVLP 371
 QY 337 GPNDALEWPNQKVTMLMLDQNN-----REHVIDAFRDPVTSSTSSFORP-----VNDMN 385
 Db 372 GAFNLLWPPFARVTRFSLDDQSDPGLAKPOHVTETPHDPNWKNFQKPGTWRGSLDESS 431
 QY 386 IASGCPFLCPVSKME-AKNSYVRDDAIFIKAIIVDL 419
 Db 432 LGFGVPEF--ISHQDIRKKNYVRDDAVFIRA VEL 464
 RESULT 10
 S71821
 probable interleukin 1 signal-transducing protein TRAF6 - human
 C:Species: Homo sapiens (man)
 C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S71821; S78550
 R:Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.
 Nature 383, 443-446, 1996
 A>Title: TRAF6 is a signal transducer for interleukin-1.
 A:Reference number: S71821; MUID:96434892; PMID:8837778
 A:Accession: S71821
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-522 <CAO>
 A:Cross-references: UNIPROT:Q9Y4K3; EMBL:U78798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426
 R:Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: S78550
 A:Accession: S78550
 A:Molecule type: mRNA
 A:Residues: 1-275, 'A', 277-522 <CAW>
 A:Cross-references: EMBL:U78798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426
 C:Genetics:
 C:Function:
 A:Description: activates transcription factor NF-kappa-B in response to interleukin-1
 A>Note: interleukin-1 induces the association of TRAF6 with the IRAK serine/threonine kinase
 C:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 F;66-114/Domain: RING finger homology <RRN>
 Query Match 18.5%; Score 408; DB 2; Length 522;
 Best Local Similarity 24.4%; Pred. No. 2.3e-22;
 Matches 117; Conservative 70; Mismatches 159; Indels 134; Gaps 15;
 QY 28 LEAKYLCSACRNVRPFPQACQGRHYCSFCLASILSSGPNQCAACVHEGIEGSIILES 87
 Db 64 LESKYECPICLMALEAREAVQTCGHRFCACIKSIRDAGHKCPV-----DNEILLE 114
 QY 88 SSAPPDNAAREVSLPAVCSDGCTWKTGLKEYFQDH-----VKTCKCR-----134
 Db 115 NQLPDPNFAKEIILSLMVKCPNEGCLHKLHLE--DHQAHCFALMDCPCQCPQK 172
 QY 135 -----134
 Db 173 HNIHLKDCPRQVSCDNCASMAFEDKEIHDQNCPLANVICVNTILIREQMPNHYD 232
 QY 135 -----VPCRFHAIGCLETVEGEKQOEHEVQWLEHRLHMLSSVLEAKPLIGQSHAGS 187

Db 233 LDCPTAPICPTSTFGCEKMQRNHLARHQENTQSHMRLAQPV-HSLSVIPDSGYI-- 289
 QY 188 ELLQRCESLEKKTATFENIVCLAREVERVAMTAACSRHRLDQ--DKIALSKVQOL 245
 Db 290 -----SEVRNFQSTIHOEGLRVR-----QDHOIRLTAQMETQSMYSEL 330
 QY 246 ERSIGLKDLAVADLQKQVLEASTYDGVFIWKISDFARKLQEAQVAGRIPAFSPAFVTS 305
 Db 331 KRTI-----RTLEDKVAIEAQOCNGIYIWKIGNFGMLKCOEERKPVVHSPGYTG 383
 QY 306 RYGYKMCRIYINGDGTGR-GTHLSLFVVMKGPNDALLRPPFNQKVTMLLDQN----- 359
 Db 384 KPGYKLCMLRLHQLPTAQRCAANYISLFTVHTMQGEYDLSLPPFPGTGLRLTLDQSEAPVR 443
 QY 360 -NREHVIDAFRDPVTSSTSPQFVNDMLAS-GCPLFCFVSKQEAKNYSVRDDAIFKAIV 417
 Db 444 QNHHEIMDA-KPELL--AFQRTPIPRNPKGYVTFMHEALR-QRTFIKDDTLILVRCEV 499

RESULT 11
 T22238
 A:Gene: CESP:F45G2.6
 A:Map position: 3
 A:Introns: 94/2; 119/3; 201/3; 223/3; 249/1; 277/3; 300/3; 327/3; 350/1; 395/3; 448/3
 A:Superfamily: TNF receptor-associated factor (TRAF); RING finger homology
 F:161-107/Domain: RING finger homology <RR>
 Query Match 17.9%; Score 395; DB 2; Length 509;
 Best Local Similarity 26.7%; Pred. No. 2e-21;
 Matches 117; Conservative 65; Mismatches 171; Indels 86; Gaps 16;

QY 28 LEAKYLSACRNVLRRPQAOAGHRYCSFCLASITLSSGPQNCACVHEGYBEGISILES 87
 Db 59 LPADCTCPICQALRDPILKNCDDHYCRQCPEN--ENRTPGCAACQ-----TTIQP 107
 QY 88 SSAPFDNAAREVESLPAVC--PSDGCTWGT-----LKEYFQDHVKTGKGC----- 133
 Db 108 ELCOHRAKQKQIALPVCTTFESSGGPDQGLTLDHDLSECTFKSLK-CEKCGQFA 166
 QY 134 -----RVCPRFHAIGCTEVEGEKQOEHEVQWMLREHLAVLLSSVLEAKPLL 179
 Db 167 KNDLEKHKRAKELNRAVGSF---CNKTIKRDREHPKTPCQVVIISCPFCQGLTDRPL 222
 QY 180 GDQSHAGSELLQRCESLEKKTATFENIVCLNREVERVAMTAACSRHRLDQ----- 232
 Db 223 BIEAHCPB-----CPNVD-NVCPVPFGCTTAGKESI-----QQHLSDEPVRHLMY 268
 QY 233 ---DKIEALSKVQOLERSIGLKDLAMADLEOKVLEMASTYDGVF-----IWKISDFARKL 286
 Db 269 LCDEITDLKGYVELMERDMG---SFNDQRTILS-AAETCTEMFGQLLWKIDKLQRT 323
 QY 287 QEAQVAGRIPAFSPAFVTSRYGYKMCRIYINGDGTGRGTHLSLFFVVMKGPNDALLRWP 346
 Db 324 NEAKSGADTTIFSVFVMSHREGYKQMAACFLFGDGAGKISLYVLLKRGFDPTLEWP 383
 QY 347 FNQKVTMLLDQN-----NREHVIDAFRDPVTSSTSPQFVNDMLIASGCPLFCFVSKM 399
 Db 384 FHRAIKISLLDQNPREDRVNITVDPKRLKANEKFLARPGRENAVAFSGSFCSLAIL 443

QY 400 EAKNSVVRDDAIFKAIVD 418
 Db 444 Q-----NVYKDKIYVQIDVD 459

RESULT 12
 S24134
 A:Gene: endopeptidase 2 (EC 3.4.24.-) - rat
 N:Alternate names: endopeptidase 24.18
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S24134
 R:Corbell, D.; Gaudoux, F.; Mainwright, S.; Ingram, J.; Kenny, A.J.; Boileau, G.; Crine, P.E.S. Lett. 309, 203-208, 1992
 A:Title: Molecular cloning of the alpha-subunit of rat endopeptidase-24.18 (endopeptidase
 A:Reference number: S24134; MUID:92371675; PMID:1505684
 A:Accession: S24134
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-748 <COR>
 A:Cross-references: UNIPROT:Q64230; GB:S43408; NID:G254297; PIDN:AAB23030.1; PID:G254298
 C:Superfamily: meprin; astacin homology; EGF homology; MAM homology
 C:Keywords: hydrolase; metalloproteinase; zinc
 F:76-262/Domain: astacin homology <AST>
 F:265-434/Domain: MAM homology <MAM>
 F:676-711/Domain: EGF homology <EGF>
 F:156-160,166/Binding site: zinc (His) #status predicted
 F:157/Active site: Glu #status predicted

Query Match 6.3%; Score 139; DB 2; Length 748;
 Best Local Similarity 27.0%; Pred. No. 0.023; 67; Indels 34; Gaps 8;
 Matches 47; Conservative 26; Mismatches 67; Indels 34; Gaps 8;

QY 276 IWKISDFARKLQEAQVAGRIPAFVTSRYGYKMCRIYINGDGTGRGTHLSLFFVVM 335
 Db 436 VMTIRNISQVLENTVKG--DRIVSRPFVNSE-GYGFVGLYFNGRITNSGVGLAFHLY 492
 QY 336 KGPNDALLRWP-NOKVTMLLDQ-----NREHVIDAFRDPVTSSTSPQ----- 378
 Db 493 SGDNVDVILEWPEVNEQAINTILDQEPDARNMSLSLMP-----TTSKYQTSSAINGSVIMD 548
 QY 379 RPVNDMNTASGCPLFCPVS-----KMEAKNSVVRDDAIFKA-IVDLTGL 422
 Db 549 RTKVGVDYKDCDCFRSIDMGWQALSHQMLNRRNFLKDDTLILFVDFKDLTHL 602

RESULT 13
 A48040
 A:Gene: meprin A (EC 3.4.24.18) beta chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 17-Feb-2003
 C:Accession: A48040
 R:Gerpea, C.M.; Marchand, P.; Jiang, W.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Bc
 J. Biol. Chem. 268, 21035-21043, 1993
 A:Title: Cloning, expression, and chromosomal localization of the mouse meprin beta subu
 A:Reference number: A48040; MUID:94012651; PMID:8407940
 A:Accession: A48040
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-704 <GOR>
 A:Cross-references: GB:L15193
 C:Superfamily: meprin; astacin homology; EGF homology; MAM homology
 C:Keywords: hydrolase; metalloproteinase; zinc
 F:72-258/Domain: astacin homology <AST>
 F:261-430/Domain: MAM homology <MAM>
 F:611-646/Domain: EGF homology <EGF>
 F:153,157,163,212/Binding site: zinc (His, His, Tyr) #status predicted
 F:154/Active site: Glu #status predicted

Query Match 6.1%; Score 135; DB 2; Length 704;
 Best Local Similarity 25.9%; Pred. No. 0.043;
 Matches 45; Conservative 35; Mismatches 54; Indels 40; Gaps 10;

QY	276	INKISDPARKLOEAVAGRIPAI	PAIFSPAFVTSRYGYMKCLR	RIYLXGDCDGRGRTHTLSL	FEVUM	335
Db	432	IWHIQNFT---	QILGGQDTSYSPFPSSK-GY-	AFQIYMD---	LYSTNTVGIVFHLI	481
QY	336	KGNDALLKWPEN-QKVTLMLLDQ	-----NNREHVIDAFPPDVTSSS	-----FQRP-	380	
Db	482	SGANDDOLQMPCEWQOANTLLDQ	NDFIRQMQRISITD	-----FTMTSDNGSYFWDRES	538	
QY	381	---VNDM-----	NIASGCLFCPCYSKMEAKNSYVRD	DAIFKAIVDLTGL	422	
Db	539	KUGVTDVFNPGTQSRGICYGTVT	ITRERLKSREFIKGDDIYILLINVED	ISHL	592	

RESULT 14
IS1055
recombination activating protein - rainbow trout
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: IS1055

R/Hansen, J.D.; Kaattari, S.L.
Immunogenetics 42, 188-195, 1995
A>Title: The recombination activation gene 1 (RAG1) of rainbow trout (*Oncorhynchus mykiss*)
A/Reference number: I51055; MUID: 95369845; PMID: 7642230
A/Accession: I51055
A/Status: preliminary; translated from GE/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-1073 <RAG>
A/Cross-references: UNIPROT:Q91187; EMBL:U15663; NID:G558917; PID:G558918
C/Genetics:
A/Gene: RAG-1
A/Introns: 489/1
C/Keywords: zinc
F:306-354/Domain: RING finger homology <RNG>

Query Match	Score	DB 2	Length
Best Local Similarity	6.0%	133.5	1073
Matches	22.2%	Pred. No. 0.092	
84; Conservative	45; Mismatches	148; Indels	101; Gaps
21;			

Qy	20	SKTLLTKLEAKYL----	CSACRNVLRRPFOAQCGHRYCSEFCILAS-ILSSGPONCAACVH	74
Db	292	SARLLSIEDLPVDFLSVTTCQVCDHLHSEPVQSPCRHLFCRSCIAKIYISLGP-HCPACT-	349	
Qy	75	EGIYESGIIILBSSAFDNNARREVESLPVPCPSDGTWKGT.LKEYEFODHVKTCGKCR	134	
Db	350	-----LPCGFADITAPAKGFLGVTHSLPLJLCPRESCQGVRLDSF-	389	
Qy	135	VPCTRHAIG-CLJETVEGE--KQOEHEVQWL-----REHLAMLJSSVLEAKPLLGDS	183	
Db	390	---RACLGHLEEVVDGDKSAENSLDNFLPVNKGGRPRQHLLSLTERRA-----QK	437	
Qy	184	HAGSELLQRCESL-EKKTATFENIVCVLNRVERVAMTAEACRQHRLDODKTEALSSVK	242	
Db	438	HLRLDLKTQVKVFAEKEGGDTKSVCV-----TLFLLLRAGNEHR-QADELEAMVQ--	488	
Qy	243	QQLERSIGLKDLAMADLEQKVLMEASTYDGVFWFKLISDFARKLOEAVAGRIAFISPAF	302	
Db	489	---GRGFGLHPVACLAIKRVNTF-LJSCSYHKMY-----RTVKATSGR-QIFQPL-532		
Qy	303	YTSRYGKMKCLRIY-----LNGDGTGRGTHSLJLFFVVMKGPNDALLEWPFENQKVTLM	354	
Db	533	HTLRTAEKLLPGYHPFEPWQPAKKSVEST-SCHVGII-----DGLSCW-----IA	575	
Qy	355	LLDÖNNREHVDAFRPDV	372	
Db	576	SVDSDSPADTVTRFRFYDV	593	

```

RESULT 15
A42908
meprin A (EC 3.4.24.18) beta chain - rat
N:Alternate names: endopeptidase-2 beta chain; meprin beta chain; meprin-a beta chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004

```

C:Accession: A42908
R:Johnson, G.D.; Hersh, L.B.
J. Biol. Chem. 267, 13505-13512, 1992
A:Title: Cloning a rat meprin cDNA reveals the enzyme is a heterodimer.
A:Reference number: A42908; MUID:92317075; PMID:1377695
A:Accession: A42908
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-668 <JOH>
A:Cross-references: UNIPROT:P28826
A:Note: sequence extracted from NCBI backbone (NCBIP:107784)
C:Superfamily: meprin; astacin homology; EGF homology; MAM homology
C:Keywords: heterodimer; hydrolase; metalloproteinase; zinc
F:72-259/Domain: astacin homology <AST>
F:261-430/Domain: MAM homology <MAM>
F:153,157,163,212/Binding site: zinc (His, His, Tyr) #status predicted
F:154/Active site: Glu #status predicted

[illegible]

Search completed: November 10, 2004, 16:29:00
Job time : 42 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 10, 2004, 16:11:42 ; Search time 195 Seconds
(without alignments)
1245.170 Million cell updates/sec

Title: US-10-018-030B-2
Perfect score: 2211
Sequence: 1 MAASVTPFGSLELLQPGFS.....NSVVRDFAIFKAIYDLTGL 422

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2168	98.1	500	2 Q72337	Q72337 homo sapien
2	2155.5	97.5	501	1 TRA2 HUMAN	Aah4662 homo sapien
3	2155.5	97.5	501	2 AAH4662	Aat27320 homo sapi
4	2155.5	97.5	501	1 AAT27320	P39429 mus musculu
5	1914.5	86.6	501	1 TRA2 MOUSE	Q8C6X9 mus musculu
6	1914.5	86.6	501	2 Q8C6X9	Q8C6Q7 mus musculu
7	1910.5	86.4	501	2 Q8C6Q7	Q7T2X2 oncorhynch
8	1256	56.8	526	2 Q7T2X2	Q90WT6 carassius a
9	1149.5	52.0	501	2 Q90WT6	Q6NRN3 xenopus lae
10	1131.5	51.2	461	2 Q6NRN3	Aah70713 xenopus l
11	1131.5	51.2	461	2 AAH70713	Q13077 homo sapien
12	733.5	33.2	416	1 TRAI HUMAN	Q60803 mus musculu
13	730	33.0	567	1 TRA3 MOUSE	Q8C6Z8 mus musculu
14	729	33.0	409	2 Q8C6Z8	P39428 mus musculu
15	727	32.9	409	1 TRAI MOUSE	Q13114 homo sapien
16	717.5	32.5	568	1 TRA3 HUMAN	Q6DEG0 brachydanio
17	690	31.2	573	2 Q6DEG0	Q00463 homo sapien
18	687.5	31.1	557	1 TRA5 HUMAN	Q8AW99 oncorhynch
19	678	30.7	576	2 Q8AW99	Q805B1 gallus gall
20	669	30.3	557	2 Q805B1	P70191 mus musculu
21	664	30.0	558	1 TRA5 MOUSE	Q7T1K2 brachydanio
22	498	22.5	470	2 Q7T1K2	Aah65969 brachydan
23	498	22.5	470	2 AAH65969	Q9BUZ4 homo sapien
24	495	22.4	470	1 TRA4 HUMAN	Q6DFG9 xenopus lae
25	487	22.0	470	2 Q6DFG9	Q8BBD9 m mus muscu
26	486	22.0	470	2 Q8BBD9	Q6DEV2 xenopus tro
27	478	21.6	470	2 Q6DEV2	Q7T1K1 brachydanio
28	471	21.3	478	2 Q7T1K1	Q61382 mus musculu
29	454.5	20.6	470	1 TRA4 MOUSE	Q70617 hydractinia
30	430.5	19.5	409	2 Q70617	Caeh8928 hydractin
31	430.5	19.5	409	2 CAE88928	

ALIGNMENTS

RESULT 1

ID	Q72337	PRELIMINARY;	PRT;	500 AA.
AC	Q72337			
DT	01-OCT-2003 (Tremblrel. 25, Created)			
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein DKFP686H1465 (Fragment).			
GN	Name=DKFP686H1465;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Human endometrium;			
RA	Ottewaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B.,			
RA	Amid C., Osanger A., Fobo G., Han M., Wiemann S.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.			
DR	EMBL; BX538160; CAD98040.1; .			
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.			
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.			
DR	GO; GO:0008270; F:zinc ion binding; IEA.			
DR	GO; GO:0001656; F:protein ubiquitination; IEA.			
DR	InterPro; IPR002083; MATH.			
DR	InterPro; IPR001841; Znf_ring.			
DR	InterPro; IPR001293; Znf_TRAF.			
DR	Pfam; PF00917; MATH; 1.			
DR	Pfam; PF00097; ZF-C3HC4; 1.			
DR	Pfam; PF02176; ZF-TRAF; 1.			
DR	SMART; SM00061; MATH; 1.			
DR	SMART; SM00184; RING; 1.			
DR	PROSITE; PS00144; MATH; 1.			
DR	PROSITE; PS00518; ZF_RING_1; 1.			
DR	PROSITE; PS00089; ZF_RING_2; 1.			
DR	PROSITE; PS00145; ZF_TRAF; 1.			
KW	Hypothetical protein; Metal-binding; Zinc; Zinc-finger.			
FT	NON TER 1			
SQ	SEQUENCE 500 AA; 55253 MW; AC9B3D7DDC4F25B3 CRC64;			
Query Match 98.1%; Score 2168; DB 2; Length 500;				
Best Local Similarity 88.4%; Pred. No. 1.5e-144;				
Matches 421; Conservative 0; Mismatches 1; Indels 54; Gaps 1;				
QY	1	MAASVTPFGSLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFOACGCHRYCSFCLAS	60	
DB	25	MAASVTPFGSLELLQPGFSKTLTGKLEAKYLSACRNVLRRPFOACGCHRYCSFCLAS	84	
QY	61	ILSSGPQACACVHEGIIYEIGISILESSAPPDNAARVESLPAVCFSDGCTWKGTIKE	120	
DB	85	ILSSGPQACACVHEGIIYEIGISILESSAPPDNAARVESLPAVCFSDGCTWKGTIKE	144	
QY	121	YE-----FQDH 126		

Db 145 YSCEHRCPLMLTECPACKGLVRLGEXERHLEHECPRESLSCHRCAPCGADVKQDH 204
QY 127 VTKCKRCVPCRFHFAIGLCTVEGSKQOEHEVQWMLREHLAMLLSVLEAKPLLDQSHAG 186
Db 205 VTKCKRCVPCRFHFAIGLCTVEGSKQOEHEVQWMLREHLAMLLSVLEAKPLLDQSHAG 264
QY 187 SELLQRCSSLEKTKATFENIVCLNREVERVAMTAACSCROHRLDQDKIEALSQVQOLE 246
Db 265 SELLQRCSSLEKTKATFENIVCLNREVERVAMTAACSCROHRLDQDKIEALSQVQOLE 324
QY 247 RSLGKDLAMADLEQKVLMEASSTYDGVFIWKISDFARFKLOEAVAGRIPAIFSPAFYTSR 306
Db 325 RSLGKDLAMADLEQKVLMEASSTYDGVFIWKISDFARFKLOEAVAGRIPAIFSPAFYTSR 384
QY 307 GYKMKCLRIYLNGDGTGRGTHLSLFFVVMKGNPDALLRPENOKVTMLLDONNREHVID 366
Db 385 GYKMKCLRIYLNGDGTGRGTHLSLFFVVMKGNPDALLRPENOKVTMLLDONNREHVID 444
QY 367 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEAKQSYVVRDDAIFIKAIIVDLTGL 422
Db 445 AFRPDVTSSSFQRPVNDMNIAAGCPLFCPVSKMEAKQSYVVRDDAIFIKAIIVDLTGL 500
RESULT 2
ID TRAF2 HUMAN STANDARD; PRT; 501 AA.
AC Q12933; Q96NT2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE TNF receptor associated factor 2 (Tumor necrosis factor type 2)
DE Receptor associated protein 3)
GN Name=TRAF2; Synonyms=TRAF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95366958; PubMed=7639698;
RA Song H.Y., Donner D.B.;
RT "Association of a RING finger protein with the cytoplasmic domain of
RT the human type-2 tumour necrosis factor receptor.";
RL Biochem. J. 309:825-829 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISUE=Cerebellum;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kimihara K., Kataoka T., Nakamura K., Kikkawa M.,
RA Yanazaki M., Nishimura K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Moniyama H., Sato N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Sato T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45 (2004).
RN [3]
RP SEQUENCE FROM N.A.
RC TISUE=Colon, Fetal brain, Kidney, Leukocyte, and Stomach;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF 201-501 FROM N.A., AND INTERACTIONS WITH TRAF1 AND
RP TNFRSF1B.
RX MEDLINE=94349371; PubMed=80669916;
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692 (1994).
RN [5]
RP REVIEW.
RX MEDLINE=21278352; PubMed=11384837;
RA Wajant H., Henkler F., Scheurich P.;
RT "The TNF-receptor-associated factor family: scaffold molecules for
RT cytokine receptors, kinases and their regulators.";
RL Cell. Signal. 13:389-400 (2001).
RN [6]
RP REVIEW.
RX MEDLINE=21519158; PubMed=11607847; DOI=10.1038/sj/onc/1204788;
RA Bradley J.R., Pober J.S.;
RT "Tumor necrosis factor receptor-associated factors (TRAFs).";
RN Oncogene 20:6482-6491 (2001).
RN [7]
RP INTERACTION WITH TNFRSF8.
RX MEDLINE=96195221; PubMed=86271180;
RA Lee S.Y., Park C.G., Choi Y.;
RT "T cell receptor-dependent cell death of T cell hybridomas mediated by
RT the CD30 cytoplasmic domain in association with tumor necrosis factor
RT receptor-associated factors.";
RL J. Exp. Med. 183:669-674 (1996).
RN [8]
RP INTERACTION WITH TANK.
RX MEDLINE=96323205; PubMed=8710854;
RA Rothe M., Xiong J., Shu H.-B., Williamson K., Goddard A.,
RA Goeddel D.V.;
RT "I-TRAF is a novel TRAF-interacting protein that regulates TRAF-
RT mediated signal transduction.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:8241-8246 (1996).
RN [9]
RP INTERACTION WITH TNFRSF14.
RX MEDLINE=97298041; PubMed=9153189;
RA Hsu H., Solovjev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
RT "ATAR, a novel tumor necrosis factor receptor family member, signals

[2]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP STRAIN=C57BL/6; TISSUE=Kidney;
 RC MEDLINE=98129826; PubMed=9461607;
 RA Brink R., Lodish H.F.;
 RX "Tumor necrosis factor receptor (TNFR)-associated factor 2A (TRAF2A),
 RT a TRAF2 splice variant with an extended RING finger domain that
 RT inhibits TNFR2-mediated NF-kappaB activation.";
 RL J. Biol. Chem. 273:4129-4134(1998).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=C57BL/6;
 RC MEDLINE=21173195; PubMed=11275257;
 RA Grech A., Quinn R., Srinivasan D., Badoux X., Brink R.;
 RX "Complete structural characterisation of the mammalian and Drosophila
 RT TRAF genes: implications for TRAF evolution and the role of RING
 RT finger splice variants";
 RL Mol. Immunol. 37:721-734(2000).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE=Breast tumor;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Teshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RX "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN INTERACTION WITH TRADD.
 RP MEDLINE=96152659; PubMed=8565075;
 RX Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
 RA "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF
 RT receptor 1 signal transduction pathways.";
 RL Cell 84:299-308(1996).
 RN [6]
 RN INTERACTION WITH TNFAIP3.
 RP MEDLINE=96270609; PubMed=8692885;
 RX Song H.Y., Rothe M., Goeddel D.V.;
 RA "The tumor necrosis factor-inducible zinc finger protein A20 interacts
 RT with TRAF1/TRAF2 and inhibits NF-kappaB activation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6721-6725(1996).
 RN [7]
 RN INTERACTION WITH TRAF1.
 RP MEDLINE=97258620; PubMed=9104814;
 RX Lee S.Y., Lee S.Y., Choi Y.;
 RA "TRAF1-interacting protein (TRIP): a novel component of the tumor
 RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
 RT that inhibits TRAF2-mediated NF-kappaB activation.";
 RL J. Exp. Med. 185:1275-1285(1997).
 CC [8]
 CC FUNCTION: Adapter protein and signal transducer that links members
 CC of the tumor necrosis factor receptor family to different
 CC signaling pathways by association with the receptor cytoplasmic
 CC domain and kinases. Association to the receptor is also mediated
 CC by the interaction with TRADD. Mediates activation of NF-kappa-B
 CC and JNK and is involved in apoptosis. Isoform 2 does not seem to
 CC mediate activation of NF-kappa-B but inhibits isoform 1 activity.
 CC The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2
 CC and BIRC3 to TNFRSF1B/TNFR2. Seems to be involved in IL-15
 CC Zinc-finger.

CC signaling (By similarity).
 CC -! SUBUNIT: Homotrimer (Probable). Heteromer with TRAF1. Binds to
 CC TNFRSF1B/TNFR2, TNFRSF4 and TNFRSF5/CD40 (By similarity).
 CC Associates with TNFRSF7/CD27, TNFRSF8/CD30, TNFRSF9/CD137,
 CC TNFRSF11A/RANK, TNFRSF13B/TAC1, TNFRSF14, TNFRSF16/NGFR,
 CC TNFRSF17/BCMA, TNFRSF18/AT1R, TNFRSF19/TROY, TNFRSF19/RELT,
 CC XEDAR, EDAR, IL15RA, TANK/ITRAF, RIPK2, TNK1, MAP3K14, MAP3K5,
 CC MAP3K1, MAP4K2, CDK9, CSK, and TRAF and TNF receptor associated
 CC protein TRAF2 (By similarity). Interacts with TNFAIP3. Binds to
 CC TRADD. Interacts with BIRC2 and BIRC3 N-terminus. Interacts with
 CC CYLD (By similarity).
 CC -! SUBCELLULAR LOCATION: Cytoplasmic.
 CC -! ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P39429-1; Sequence=Displayed;
 CC Name=2; Synonyms=TRAF2A;
 CC IsoId=P39429-2; Sequence=VSP_007402;
 CC Note=NC experimental confirmation available. On mRNA level, has
 CC a significantly shorter half-life than isoform 1;
 CC -! TISSUE SPECIFICITY: Isoform 1 and isoform 2 are expressed in
 CC spleen, adipose tissues, skeletal muscles, thymus, testis, heart,
 CC lung, brain. Isoform 2 is very weakly expressed in heart, lung and
 CC brain.
 CC -! DOMAIN: The coiled coil domain mediates homo- and hetero-
 CC oligomerization.
 CC -! DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
 CC domains.
 CC -! PTM: Ubiquitinated; mediated by SIAH2 and leading to its
 CC subsequent proteasomal degradation. Not ubiquitinated by SIAH1 (By
 CC similarity).
 CC -! SIMILARITY: Contains 1 MATH domain.
 CC -! SIMILARITY: Contains 1 RING-type zinc finger.
 CC -! SIMILARITY: Contains 2 TRAF-type zinc fingers.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L35303; AAC37662.1; --
 CC EMBL; AF027570; AAC3545.1; --
 CC EMBL; AF233332; AAF59928.1; --
 CC EMBL; AF233326; AAF59928.1; JOINED.
 CC EMBL; AF233337; AAF59928.1; JOINED.
 CC EMBL; AF233328; AAF59928.1; JOINED.
 CC EMBL; AF233329; AAF59928.1; JOINED.
 CC EMBL; AF233330; AAF59928.1; JOINED.
 CC EMBL; AF233331; AAF59928.1; JOINED.
 CC EMBL; AF233333; AAF59928.1; JOINED.
 CC EMBL; BC003801; AAH03801.1; --
 CC PIR; I61512; I61512.
 CC HSP; Q12933; 1CA9.
 CC MGD; MGI:101635; Traf2.
 CC GO; GO:0005515; F:protein binding; IPI.
 CC GO; GO:0006916; P:anti-apoptosis; NAS.
 CC InterPro; IPR002083; MATH.
 CC InterPro; IPR008974; Traf-like.
 CC InterPro; IPR001841; Znf_zing.
 CC InterPro; IPR001293; Znf_TRAF.
 CC Pfam; PF00917; MATH; 1.
 CC Pfam; PF00097; Zf-C3HC4; 1.
 CC Pfam; PF02176; ZF-TRAF; 1.
 CC SMART; SM00061; MATH; 1.
 CC SMART; SM00184; RING; 1.
 CC PROSITE; PS01444; MATH; 1.
 CC PROSITE; PS00518; ZF_RING_1; 1.
 CC PROSITE; PS00089; ZF_RING_2; 1.
 CC PROSITE; PS01455; ZF_TRAF; 2.
 CC Alternative splicing; Apoptosis; Coiled coil; Repeat; Ubl conjugation;
 CC Zinc-finger.

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FT ZN FING 34 73 RING-type.
FT ZN FING 124 180 TRAP-type 1.
FT ZN FING 177 233 TRAP-type 2.
FT ZN FING 298 348 Coiled coil (Potential).
FT DOMAIN 351 496 MATH.
FT VARGPLIC 62 62 L -> LRCASILIS (in isoform 2).
FT FTID=VSP 007402.
SQ SEQUENCE 501 AA; 56026 MW; 043B391180365F10 CRC64;

Query Match
Best Local Similarity 86.6%; Score 1914.5; DB 1; Length 501;
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPGSLLELLQPGFSKTLGLKLEAKYLCACRNVLRRPFOACGHRYSFCLAS 60
DB 1 MAASVTPGSLLELLQPGFSKTLGLTRLEAKYLCACNVLRRPFOACGHRYSFCLTS 60

QY 61 ILSSGPQCAACVHGGIYVEEGISILESSAPFDNAAREVESLPAVCPDCTWKGTLKE 120
DB 61 ILSSGPQCAACVHGGIYVEEGISILESSAPFDNAAREVESLPAVCPDCTWKGTLKE 120

QY 121 YE----- 122
DB 121 YSCEHGLCPFLLTCPACKGLVRLSEKHEHTEQCPKRSLSOCHCAPSHVDLEVHYE 180
DB 123 -----FQDHVKTGCRKVPVCRFRHAGICLETVEGEKQHEVQWL 161
DB 181 VCPKPEPLTCDGCKKKIPRETQDHVRAKSCRVLCRFHTVGCSEMVETENLQHEQLRL 240

QY 162 REHLAMILLSSVLEAKPLGDOSHAGSELLOKCELEKKTATFENIVCVLREVERVAVTA 221
DB 241 REHLAMILLSSVLEAKPLGDOSHAGSELLOKCELEKKTATFENIVCVLREVERVAVTA 300

QY 222 EACSRQHELDQDKIBALSSKVKQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 281
DB 301 EACSRQHELDQDKIBALSSKVKQLERSIGLKDLMADLEQKVLMEASTYDGVFIWKISD 360

QY 282 FARKLOEAVAGRIPAIFSPAPYTSRYGKGLRILYNGDGTGRGTHLSLFFVVMKGNDA 341
DB 361 FTRKQEAAGVAGRTPAIFSPAPYTSRYGKGLRILYNGDGTGRGTHLSLFFVVMKGNDA 420

QY 342 LLRPFQKVTMLLDQNNRHSHVDADRPDVTSSSFQPVNDMMNIAAGCPLFCFVPSKWEA 401
DB 421 LLQPFQKVTMLLDQNNRHSHVDADRPDVTSSSFQPVNDMMNIAAGCPLFCFVPSKWEA 480

QY 402 KNSVYRDDAIFIKAVDITGL 422
DB 481 KNSVYRDDAIFIKAVDITGL 501

RESULT 6
ID Q8C6X9 PRELIMINARY; PRT; 501 AA.
AC Q8C6X9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
DE library, clone:DB30048A10 product:Tnf receptor-associated factor 2,
DE full insert sequence.
GN Name=Traf2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:11617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imctani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AK052934; BAC35209.1; -.
DR HSSP; Q12933; 1CA9.
DR MGD; MGI:101835; Traf2.
DR GO; GO:0001513; Cubiquitin ligase complex; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR GO; GO:0004842; F-ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.
DR GO; GO:0016567; P-protein ubiquitination; IEA.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf-like.
DR InterPro; IPR001841; Znf_Fing.
DR InterPro; IPR001293; Znf_TRAF.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00097; ZF-C3HC4; 1.
DR Pfam; PF02176; ZF-TRAF; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.

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DR PROSITE; PS50145; ZF TRAF; 2.  
KW Metal-binding; Receptor; Zinc; Zinc-finger.  
SQ SEQUENCE 501 AA; 56086 MW; 89DDCB17782BBF1F CRC64;  
  
Query Match 86.4%; Score 1914.5; DB 2; Length 501;  
Best Local Similarity 74.3%; Pred. No. 1.2e-126;  
Matches 372; Conservative 21; Mismatches 29; Indels 79; Gaps 1;  
  
QY 1 MAAASVTPGSLLELPGSKTLGKLEAKYLCSACRNLRRPFOACQGHYVSPFCILAS 60  
DB 1 MAAASVTPGSLLELPGSKTLGKLEAKYLCSACKNLRPPFOACQGHYVSPFCILTS 60  
QY 61 ILSSGPNCAACVHEGIIYEGISILSSSAFPDPAARREVESLPAYCPDGGTGWGTLE 120  
DB 61 ILSSGPNCAACVHEGIIYEGISILSSSAFPDPAARREVESLPAYCPDGGTGWGTLE 120  
QY 121 YE----- 122  
DB 121 YESCHGLCPFLTECPACKGLVRLSEKHHTTEQCPKSLSCQHCRAFCSHVDVHVYE 180  
QY 123 -----FOCHKVTCGKCRVPCRFHAIGCLETVGEKQKEHEVQWL 161  
DB 181 VCPKFPITYDVGCGKKIPRETFOHVRACSKCRVLCRFHTVGCSENVETENIQDELQRL 240  
QY 162 REHLAMLLSVLEAKPLGDQSHAGSELLQRCBSLEKKTATTENIVCVLNREVERVAVTA 221  
DB 241 REHLAALLSFLSAQASPTLNQVPELLQRCQILEKTIATTENIVCVLNREVERVAVTA 300  
QY 222 EACSRQHRLLDODKIEALSSKVOQLERSIGLKDLAVADLSQKLEMEASTYDGVFTWKISD 281  
DB 301 EACSRQHRLLDQKIEALSINKVOQLERSIGLKDLAVADLSQKLEMEASTYDGVFTWKISD 360  
QY 282 FARKLQEAAGVGRIPAFIPSPAFYTSRYGVKVCRIYVNGDGTGRGTHLSLFFVVMKGPND 341  
DB 361 FTRKQEAAGVGRIPAFIPSPAFYTSRYGVKVCRIYVNGDGTGRGTHLSLFFVVMKGPND 420  
QY 342 LLEWPNQKVTMLLDNNRHHVIDAFRDPDVTSSSPQRPVNDMTASGCLPFCPSKMEA 401  
DB 421 LQWPNQKVTMLLDNNRHHVIDAFRDPDVTSSSPQRPVNDMTASGCLPFCPSKMEA 480  
QY 402 KNSYVRDDAIFIKAIVDLTGL 422  
DB 481 KNSYVRDDAIFIKAIVDLTGL 501  
  
RESULT 7  
Q8CAQ7 PRELIMINARY; PRT; 501 AA.  
AC Q8CAQ7  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched  
DE library, clone:Al30081B14 product:Tnf receptor-associated factor 2,  
DE full insert sequence.  
GN Name=Traf2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=21055660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
  
RL Nature 409:685-690(2001).  
RN [3]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RA The FANTOM Consortium,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20493974; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RN SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuchi S., Furuno M., Hasegaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imoani K., Ishii Y., Itoh M., Kigawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akai S., Takeda Y., Tanaka I.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RL -!- SIMILARITY: Contains 1 RING-type zinc finger.  
CC EMBL; AK038136; BAC29937.1; -.  
DR HSSP; Q12933; 1CA9.  
DR MGD; MGI:101835; Traf2.  
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR GO; GO:0016567; P:protein ubiquitination; IEA.  
DR InterPro; IPR002083; MATH.  
DR InterPro; IPR008974; Traf-like.  
DR InterPro; IPR001841; Znf-fing.  
DR InterPro; IPR001293; Znf-TRAF.  
DR Pfam; PF00917; MATH; 1.  
DR Pfam; PF00097; zf-C3HC4; 1.  
DR Pfam; PF02176; zf-TRAF; 1.  
DR SMART; SM00061; MATH; 1.  
DR SMART; SM00184; RING; 1.  
DR PROSITE; PS50144; MATH; 1.  
DR PROSITE; PS00518; ZF RING 1; 1.  
DR PROSITE; PS00089; ZF RING 2; 1.  
DR PROSITE; PS50145; ZF TRAF; 2.  
KW Metal-binding; Receptor; Zinc; Zinc-finger.  
SQ SEQUENCE 501 AA; 56026 MW; EB219C117A935FEA CRC64;  
  
Query Match 86.4%; Score 1910.5; DB 2; Length 501;
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Best Local Similarity 74.1%; Pred. No. 2.2e-126;
Matches 371; Conservative 22; Mismatches 29; Indels 79; Gaps 1;

QY 1 MAASVTPGSLLELPQFSKTLTGKLEAKYLCACNVLRPFQACGHRYSFCLAS 60
Db 1 MAASVTPGSLLELPQFSKTLTGKLEAKYLCACNVLRPFQACGHRYSFCLAS 60
QY 61 ILSSGPQCAACVHGIYEEGISELESSAFPDNAARREVESLPAVCPDGTWKGTKE 120
Db 61 ILSSGPQCAACVHGIYEEGISELESSAFPDNAARREVESLPAVCPDGTWKGTKE 120
QY 121 YE----- 122
Db 121 YESCHEGLCPFLTECPACKGLVRLSEKHEHTBECPRKSLSCOHCRAPCSHVLDLHYE 180
QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVEGEKQHEVQWL 161
Db 123 -----FQDHVKTGCKRVPFCRFAIGCLTVEGEKQHEVQWL 161
QY 181 VCPKPLTCDGCGKKIPRETQDHVRAKSCRVLCRFHTVGCSEMVETENLQDHELQRL 240
Db 181 VCPKPLTCDGCGKKIPRETQDHVRAKSCRVLCRFHTVGCSEMVETENLQDHELQRL 240
QY 162 REHLAMLSVLEAKPLLDGSHAGSELLORCESLEKKTATFENIVCVLREVERVAVTA 221
Db 162 REHLAMLSVLEAKPLLDGSHAGSELLORCESLEKKTATFENIVCVLREVERVAVTA 221
QY 241 REHLALLSSLEAQAASPTNQVPELLOQCILEQKIATFENIVCVLREVERVAVTA 300
Db 241 REHLALLSSLEAQAASPTNQVPELLOQCILEQKIATFENIVCVLREVERVAVTA 300
QY 222 EACSRQHLDDKIBALSKVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISD 281
Db 222 EACSRQHLDDKIBALSKVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISD 281
QY 301 EACSRQHLDDKIBALSKVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISD 360
Db 301 EACSRQHLDDKIBALSKVQQLERSIGLKDAMADLEQKVLMEASTYDGVFIWKISD 360
QY 282 FARKLOEAVAGRIPAIFSPAFYTSRYGYMCLRIYLNQDGTGRGTHLSLFFVVMKGNDA 341
Db 282 FARKLOEAVAGRIPAIFSPAFYTSRYGYMCLRIYLNQDGTGRGTHLSLFFVVMKGNDA 341
QY 361 FTRKQEAQVAGRTAIFSPAFYTSRYGYMCLRIYLNQDGTGRGTHLSLFFVVMKGNDA 420
Db 361 FTRKQEAQVAGRTAIFSPAFYTSRYGYMCLRIYLNQDGTGRGTHLSLFFVVMKGNDA 420
QY 342 LLRWPFNKQVTLMLLDONNREHVIDAFRPDVTSSSFQRPVNDMNIAGCPLFCPVSKMEA 401
Db 342 LLRWPFNKQVTLMLLDONNREHVIDAFRPDVTSSSFQRPVNDMNIAGCPLFCPVSKMEA 401
QY 421 LLWPFNKQVTLMLLDONNREHVIDAFRPDVTSSSFQRPVNDMNIAGCPLFCPVSKMEA 480
Db 421 LLWPFNKQVTLMLLDONNREHVIDAFRPDVTSSSFQRPVNDMNIAGCPLFCPVSKMEA 480
QY 402 KNSVYRDDAIFIKAVIDLTLGL 422
Db 402 KNSVYRDDAIFIKAVIDLTLGL 501

RESULT 8
QY72X2 PRELIMINARY; PRT; 526 AA.
AC QY72X2;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Tumor necrosis factor receptor associated factor 2.
GN Name=TRAF2;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]_TaxID=8022;
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Zou J., Zhang Y., Seconbes C.J.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AJ548839; CAD59021.2;
DR GO; GO:0000131; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002083; MATH_
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF02176; zf-TRAF; 2.

Best Local Similarity 56.8%; Score 1256; DB 2; Length 526;
Best Local Similarity 47.5%; Pred. No. 3.4e-80;
Matches 250; Conservative 68; Mismatches 100; Indels 108; Gaps 5;

QY 4 ASVTTPGSLLELPQFSKTLTGKLEAKYLCACNVLRPFQACGHRYSFCLAS 63
Db 2 ARISLP-SLDSLPRIPOSVLAVSEAKYQCCQHVLRKPVQACGHRFCVCFKLTLS 60
QY 64 SGPQNCACVHGIYEEGISELESSAFPDNAARREVESLPAVCPDGTWKGTKE- 122
Db 61 SGPKEACRQBEIYEEPSILNSNEAFPDNAAGREIASLPAKCISEGSWTGCIKEYEA 120
QY 123 ----- 122
Db 121 QHEGKDYERVPCTCQVLLRSEKERHNERCEARTLNCKYKVSFNFKEIKAHDEICQ 180
QY 123 -----FQDHVKTGCKRVPFCRFAIGCLTVEGEKQHEVQWLREH 164
Db 181 KFPMQCKGCKKKIPREKFLDHSRSCAKSKTACPFSEVGCKVIIDNGKHSDEQTSVNEH 240
QY 165 LAMLSVLEAK-----PLIGD-QSHAGSELLORCE-----SL 196
Db 241 LRLILATLSVLQRLQPEAPGLCEWQEDSGGLYRAPEDGATAIATDGGAAASQTEGL 300
QY 197 EKTATFENIVCVLREVERVAVTAACSRQHLDDKIBALSKVQQLERSIGLKDAM 256
Db 301 DHKVRALFNIVCVLREVERVAVTAACSRQHLDDKIBALSKVQQLERSIGLKDAM 360
QY 257 ADLEQKVLMEASTYDGVFIWKISDFARKLOEAVAGRIPAIFSPAFYTSRYGYMCLRIY 316
Db 361 AETDQTLRELQCTFDGVFVWKIADFSSRRQDAVAGRTAPAMFSPAFYTSRYGYMCLRIY 420
QY 317 LNGDGTGRGTHLSLFFVVMKGNDAIIFIKAVIDLTLGL 422
Db 421 LNGDGTGRGTHLSLFFVVMKGNDAIIFIKAVIDLTLGL 480
QY 377 FORPVNDMNIAGCPLFCPVSKMEAKNSVYRDDAIFIKAVIDLTLGL 526
Db 481 FLRPNEMNIAGCPLFCPLAKGSSYLDDTIFIKAVIDLTLGL 526

RESULT 9
QY90WT6 PRELIMINARY; PRT; 501 AA.
AC QY90WT6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor associate factor-2.
GN Name=traf2;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]_TaxID=7957;
RP SEQUENCE FROM N.A.
RA Wang T., Seconbes C.J.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AJ297860; CAC82653.1; -.
DR HSSP; Q12933; 1CZV.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.

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GO; GO:0004842; Fubiquitin-protein ligase activity; IEA.
GO; GO:0008270; Fzinc ion binding; IEA.
GO; GO:0016567; P;protein ubiquitination; IEA.
InterPro; IPR002063; MATH.
InterPro; IPR008974; Traf-like.
InterPro; IPR001841; Znf_Traf.
InterPro; IPR001293; Znf_Traf.
Pfam; PF00917; MATH; 1.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF02176; zf-TRAF; 2.
SMART; SM00061; MATH; 1.
SMART; SM00184; RING; 1.
PROSITE; PS50144; MATH; 1.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50145; ZF-TRAF; 2.
KW Metal-binding; Receptor; Zinc; Zinc-finger.
SQ SEQUENCE 501 AA; 56503 MW; DE0ED0F8D9DC287 CRC64;
Query Match 52.0%; Score 1149.5; DB 2; Length 501;
Best Local Similarity 47.8%; Pred. No. 1e-72;
Matches 226; Conservative 60; Mismatches 84; Indels 105; Gaps 4;
QY 2 AAASVTPPGSLELLQPGSKTLGLTLEAKYLCACRNVLRRPFOAQCCHRYCSFCLASI 61
DB 13 AMARPSLPSSLDSTLPGISREVLVSMEPKYQOQCKEILRKPFOAQCCHRYCFVCFKQL 72
QY 62 LSSGPQNCACVHEGIYEEGISILESSAFPNDNAARREVESLPVPCSDGCTWKGLTKEY 121
DB 73 TSSGPIPCACRAEGIFEEAMSLNITVAPPDNAARREIDSLPAKCPNDGCSWGLTKDY 132
QY 122 E----- 122
DB 133 EGOHGRCDPFRVCKACQAVILLSEKDRHRECEARTLNCKYKVTFNPKEIKAHDEI 192
QY 123 -----FQHVTKCGKRVPCRFHAGCTLVGEGKQHEVQWLRL 162
DB 193 CQKFPQCKDCGKKIPREKFOHTKSCAKSACQFSEIGCRAVVDNGKQHEQTSVM 252
QY 163 EHLAMLLSVLEAKPLIGD-----QSHAGSELLORCE-----SLE 197
DB 253 EHLRLML-SVLSVRRAEGAGQWSDSLGLYRGPDAPPAGPNAANAGRGPGVQ 311
QY 198 KKTATPENIVCVLNREVERVAMTAACSRQHRLDQDKIEALSKVQOOLERSIGLKDLAMA 257
DB 312 QKVTALENIVCVLNREVERVAMTAACSRQHRLDQDKIEALSKVQOOLERSIGLKDLAMA 371
QY 258 DLQKVLNEASTYDGVFWIKSDPAKLOEAVAGRIPIAFSPAFYTSRYGMYMCLRIYL 317
DB 372 ESQSLRELQFCTYDGVFWIKSDPAKLOEAVAGRIPIAFSPAFYTSRYGMYMCLRIYL 431
QY 318 NGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDQNNRHRVIDAFRPDV 372
DB 432 NGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTMLLDQNNRHRVIDAFRPDI 486
RESULT 10
Q6NRN3
ID Q6NRN3 PRELIMINARY; PRT; 461 AA.
AC Q6NRN3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MG83471 protein.
GN Name=MG83471;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22386257; PubMed=12477932;
MEDLINE=22386257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Narusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uscin T.B., Toshyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
"Genetic and genomic tools for Xenopus research: The NIH Xenopus
Initiative";
Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
Submitted (Mar-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; BC070713; AAH70713.1; -;
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf-like.
DR InterPro; IPR001841; Znf_Traf.
DR InterPro; IPR001293; Znf_Traf.
DR Pfam; PF00097; zf-C3HC4; 1.
DR Pfam; PF02176; zf-TRAF; 2.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR PROSITE; PS50145; ZF-TRAF_2;
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 461 AA; 51826 MW; 9981DC4C003C321D CRC64;
Query Match 51.2%; Score 1131.5; DB 2; Length 461;
Best Local Similarity 49.1%; Pred. No. 1.7e-71;
Matches 223; Conservative 56; Mismatches 70; Indels 105; Gaps 4;
QY 2 AAASVTPPGSLELLQPGSKTLGLTLEAKYLCACRNVLRRPFOAQCCHRYCSFCLASI 61
DB 7 AAVSVSPGSLDLNQPQPKKEILGTLEVKYLCSDCNLLRRPLQAQCCHRYCSHCFSKI 66
QY 62 LSSGPQNCACVHEGIYEEGISILESSAFPNDNAARREVESLPVPCSDGCTWKGLTKEY 121
DB 67 ISSGPQKCAACIQGLYEDGVSMLESSAFPNDNAARREVESLPAINVNCVTKGTKEF 126
QY 122 E----- 122
DB 127 EVGHEGKQFVLPVCPVKALIRAIARDLNNRERCPKLNCRKYLVSVPFDIKVHDEI 186
QY 123 -----FQHVTKCGKRVPCRFHAGCTLVGEGKQHEVQWLRL 162
DB 187 CPKPMTCGCGRKKIPREKFOHTKSCAKSACQFSEIGCRAVVDNGKQHEQTSVM 246
QY 163 EHLA-----MLSSVLEAKPLI-----GDQSHAGS-----ELLQRCESL 196
DB 247 EHLAKWMDYIQDIEKQKDELLLRVGSLSVQGSFGHNLFPVPNDSTKVKKEILQKDLT 306
QY 197 EKKTATPENIVCVLNREVERVAMTAACSRQHRLDQDKIEALSKVQOOLERSIGLKDLAMA 256

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Db 307 DXKTTTFKIVSVLNGKRVSWSHATEELMKQLLAAQEKVESLTKVROLEFTLQCKELVL 366
QY 257 ADLEQKVLMEASTYDGVFIWKISDFARKLOEAVAGRIPAFISPAFYTSRYGYKMCRLIY 316
Db 367 AEMGTRMQESESFTYDGVFIWKISLGLKRLDAASGRCPALFSPFFYTKYGYKMCRLIY 426
QY 317 LINGDGTGRGTHLSLFFVVMKGNPDALLRWPFPNQK 350
Db 427 LDGDTGRGTHLSLFFVVMKGNPDALLRWPFPNQK 460

RESULT 11
AAH70713
ID AAH70713 PRELIMINARY; PRT; 461 AA.
AC AAH70713;
DT 13-MAY-2004 (TrEMBLrel. 27, Created)
DT 13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OC Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski W.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the ENBL/GenBank/DBJ databases.
DR ENBL; BC070713; AAH70713.1; -
KW Hypothetical protein.
SQ SEQUENCE 461 AA; 9981DC4C003C321D CRC64;

Query Match 51.2%; Score 1131.5; DB 2; Length 461;
Best Local Similarity 45.14; Pred. No. 1.7e-71;
Matches 223; Conservative 56; Mismatches 70; Indels 105; Gaps 4;
QY 2 AAASVTPGSLLELQPGFSKTLTGKLEAKYLCASCRNVLRRPFOAQCGHRYCSFCLASI 61

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Db 7 AAVSVSPGSLDLNPGFKKEILTKLVKYLCSCKNLLRRPLQAQCCHRYCSHCFSKI 66
QY 62 LSSGPNCAACVHEGIYBEGISILSSSAFFPNAAARREVESLPVCPDGGCTWKTKLEY 121
Db 67 ISSGPKCAACTQEGLYEDVSMLESSSAFFPNAAARREVESLPAINNVNCTWKTKIEF 126
QY 122 E----- 122
Db 127 EVGHEGKQFMLVPCVKCALIRADRLHNERCEPERKLNCRCKLSVYFPDIKVHDEI 186
QY 123 -----FQDHVKTGCKRVPCEPFAIGCTVEGKQOEHEVQMLR 162
Db 187 CPKFPMTCEGCKRKIPREKFDQHIKGCRCVKPCRYAAVCAEWVENDKCLEHENKFLA 246
QY 163 EHIA-----MLSSVLEAKFLL---GQSHAGS-----ELLQRCESL 196
Db 247 EHLAKVWDYIQDRIKEQKDLLLRVGLSVQSSSTPGHNALPVPPNDSTKVKRILQKLDL 306
QY 197 EKKTATFENIVCVINREVERVANTAEACSRQHLRDQDKIEALSSKVQOLERSIGHKDLAM 256
Db 307 DKKTTFEIVSVLNGKRVSWSHATEELMKQLLAAQEKVESLTKVROLEFTLQCKELVL 366
QY 257 ADLEQKVLMEASTYDGVFIWKISDFARKLOEAVAGRIPAFISPAFYTSRYGYKMCRLIY 316
Db 367 AEMGTRMQESESFTYDGVFIWKISLGLKRLDAASGRCPALFSPFFYTKYGYKMCRLIY 426
QY 317 LINGDGTGRGTHLSLFFVVMKGNPDALLRWPFPNQK 350
Db 427 LDGDTGRGTHLSLFFVVMKGNPDALLRWPFPNQK 460

RESULT 12
TRAI_HUMAN
ID TRAI_HUMAN STANDARD; PRT; 416 AA.
AC Q13077; OSNF13;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TNF receptor associated factor 1 (Epstein-Barr virus-induced protein
DE 6).
GN Name=TRAF1; Synonyms=EBI6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoma;
RX MEDLINE=95163092; PubMed=7859281;
RA Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,
RA Kieff E.;
RT "The Epstein-Barr virus transforming protein LMP1 engages signaling
RT proteins for the tumor necrosis factor receptor family.";
RL Cell 80:389-399(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen.";
RL Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski W.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the ENBL/GenBank/DBJ databases.
DR ENBL; BC070713; AAH70713.1; -
KW Hypothetical protein.
SQ SEQUENCE 461 AA; 9981DC4C003C321D CRC64;

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [4]
 RP REVIEW
 RX MEDLINE=21278352; PubMed=11384837;
 RA Wajant H., Henkler F., Scheurich P.;
 RT "The TNF-receptor-associated factor family: scaffold molecules for
 RT cytokine receptors, kinases and their regulators.";
 RL Cell. Signal. 13:389-400(2001).
 RL [5]
 RP REVIEW
 RX MEDLINE=21519158; PubMed=11607847; DOI=10.1038/sj/onc/1204788;
 RA Bradley J.R., Fober J.S.;
 RT "Tumor necrosis factor receptor-associated factors (TRAFs).";
 RL Oncogene 20:6482-6491(2001).
 RL [6]
 RP INTERACTIONS WITH TRAF2 AND TNFRSF1B.
 RX MEDLINE=94349371; PubMed=8069916;
 RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
 RT "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
 RL Cell 78:681-692(1994).
 RL [7]
 RP INTERACTION WITH TANK.
 RX MEDLINE=96323205; PubMed=8710854;
 RA Rothe M., Xiong J., Shu H.-B., Williamson K., Goddard A.,
 RA Goeddel D.V.;
 RT "TRAF is a novel TRAF-interacting protein that regulates TRAF-
 RT mediated signal transduction.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8241-8246(1996).
 RL [8]
 RP INTERACTION WITH TNFRSF5.
 RX MEDLINE=98384149; PubMed=9718306; DOI=10.1021/b981067g;
 RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
 RA Kehry M.R.;
 RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
 RT interactions: regulation of CD40 signaling through multiple TRAF
 RT binding sites and TRAF hetero-oligomerization.";
 RL Biochemistry 37:11836-11845(1998).
 RL [9]
 RP INTERACTION WITH RIPK2.
 RX MEDLINE=98381580; PubMed=9705938;
 RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
 RA Mattmann C., Tschopp J.;
 RT "Identification of CARDIAK, a RIP-like kinase that associates with
 RT caspase-1.";
 RL Curr. Biol. 8:885-888(1998).
 RL [10]
 RP INTERACTION WITH TNFRSF8.
 RX MEDLINE=96195221; PubMed=8627180;
 RA Lee S.Y., Park C.G., Choi Y.;
 RT "T cell receptor-dependent cell death of T cell hybridomas mediated by
 RT the CD30 cytoplasmic domain in association with tumor necrosis factor
 RT receptor-associated factors.";
 RL J. Exp. Med. 183:669-674(1996).
 RL [11]
 RP INTERACTION WITH RIPK2.
 RX MEDLINE=98307936; PubMed=9642260;
 RA McCarthy J.V., Ni J., Dixit V.M.;
 RT "RIP2 is a novel NF-kappaB-activating and cell death-inducing
 RT kinase.";
 RL J. Biol. Chem. 273:16968-16975(1998).
 RL [12]

RP INTERACTIONS WITH TNFRSF4 AND TNFRSF9.
 RX MEDLINE=98078711; PubMed=9418902;
 RA Arch R.H., Thompson C.B.;
 RT "4-1BB and Oxa40 are members of a tumor necrosis factor (TNF)-nerve
 RT growth factor receptor subfamily that bind TNF receptor-associated
 RT factors and activate nuclear factor kappaB.";
 RL Mol. Cell. Biol. 18:558-565(1998).
 RL [13]
 RP INTERACTION WITH TNFRSF9.
 RX MEDLINE=98270914; PubMed=9607925;
 RA Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
 RA Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
 RA Watts T.H.;
 RT "CD28-independent, TRAF2-dependent costimulation of resting T cells by
 RT 4-1BB ligand.";
 RL J. Exp. Med. 187:1849-1862(1998).
 RL [14]
 RP INTERACTION WITH TNFRSF11A.
 RX MEDLINE=98447691; PubMed=9774460;
 RA Wong B.R., Josien R., Lee S.Y., Vologodskaja M., Steinman R.M.,
 RA Choi Y.;
 RT "The TRAF family of signal transducers mediates NF-kappaB activation
 RT by the TRANCE receptor.";
 RL J. Biol. Chem. 273:28355-28359(1998).
 RL [15]
 RP INTERACTION WITH TNFRSF18.
 RX MEDLINE=99156876; PubMed=10037686;
 RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
 RA Liu D., Wang S.-X., Kwon B.S.;
 RT "Identification of a novel activation-inducible protein of the tumor
 RT necrosis factor receptor superfamily and its ligand.";
 RL J. Biol. Chem. 274:6056-6061(1999).
 RL [16]
 RP INTERACTION WITH TNFRSF17.
 RX MEDLINE=20363816; PubMed=10903733;
 RA Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C.,
 RA Inoue J.-I., Devergne O., Tsapis A.;
 RT "TNF receptor family member BCMA (B cell maturation) associates with
 RT TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
 RT activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-
 RT activated protein kinase.";
 RL J. Immunol. 165:1322-1330(2000).
 RL [17]
 RP INTERACTION WITH TNFRSF19.
 RX MEDLINE=20270246; PubMed=10809768;
 RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
 RT "TAF, a novel member of the tumor necrosis factor receptor family,
 RT activates the c-Jun N-terminal kinase pathway and mediates caspase-
 RT independent cell death.";
 RL J. Biol. Chem. 275:15336-15342(2000).
 RL [18]
 RP INTERACTION WITH TNFRSF19L.
 RX MEDLINE=21213541; PubMed=11313261;
 RA Sica G.L., Zhu G., Tamada K., Liu D., Ni J., Chen L.;
 RT "RELt, a new member of the tumor necrosis factor receptor superfamily,
 RT is selectively expressed in hematopoietic tissues and activates
 RT transcription factor NF-kappaB.";
 RL Blood 97:2702-2707(2001).
 RL [19]
 RP INTERACTION WITH EDAR.
 RX MEDLINE=21264720; PubMed=11035039; DOI=10.1074/jbc.M008356200;
 RA Kumar A., Eby M.T., Sicha S., Jasmin A., Chaudhary P.M.;
 RT "The ectodermal dysplasia receptor activates the nuclear factor-
 RT kappaB, UNK, and cell death pathways and binds to ectodysplasin A.";
 RL J. Biol. Chem. 276:2668-2677(2001).
 RL [20]
 RP FUNCTION: Adapter protein and signal transducer that links members
 CC of the tumor necrosis factor receptor family to different
 CC signaling pathways by association with the receptor cytoplasmic
 CC domain and kinases. Mediates activation of NF-kappa-B and JNK and
 CC is involved in apoptosis. The TRAF1/TRAF2 complex recruits the
 CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
 CC -! SUBUNIT: Homotrimer (Probable). Heteromer with TRAF2 and
 CC associates with TNFRSF1B/TNFR2 through TRAF2. Associates with

```
CC TNFRSF4, TNFRSF5/CD40, TNFRSF6/CD30, TNFRSF9/CD137,
CC TNFRSF11A/RANK, TNFRSF18/ATRA, TNFRSF17/BCMA, TNFRSF19/TROY,
CC TNFRSF19L/RELT, XEDAR, EDAR, Epstein-Barr virus ENFL1/LMP-1,
CC TANK/ITRAF, TRAF and RIPK2. Interacts with BIRC2 and BIRC3 N-
CC terminus.
CC -!- DOMAIN: The coiled coil domain mediates homo- and hetero-
CC oligomerization.
CC -!- DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
CC domains.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 111.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
Query Match 33.2%; Score 733.5; DB 1; Length 416;
Best Local Similarity 37.8%; Pred. No. 1.8e-43;
Matches 156; Conservative 65; Mismatches 109; Indels 83; Gaps 6;
CC 55 SFCLASILSSGPQN-----CAACVHEGIIYEGISILESSAPFPDAAARREVESLPVCPSS 109
CC 35 ALCCAGCLSENPRNGEDQICPKRGEDL-----QSISPGSLRLTQKAHPEV--- 81
CC 110 DCTWKGTILKEYFDFDHVTKCKRVPKCPRAIGCLEIVGEKQGEHEVQWLREHLMLL 169
CC 82 -----AEAGIGCPFAGVCGSPKSPQSQVQGEHEVTSQTSHLMLL 120
CC 170 SSVLEAKPLLDQSHAGSELLQ-----CE----- 194
CC 121 GPMKQKARLGGLESGLPMALQNLSDLOQAAVEVAGDLEVCYRAPCSQSEBELALQH 180
CC 195 -----SLKKYATFNIVCLNREVERVAMTAECRSRHRDQDKIEALSKVQOOLE 246
CC 181 FMKEXLLAELEGLKRVFNIVAVLNKEVEAGSHALATSIHOSQDRERILSLQEVVVELQ 240
CC 247 RSGIKDLAMADLEQVLEMASTYDGVFIWKISDFARKLEAVAGRIPAFISPAFYTSR 306
CC 241 QTLAQKDALGLKLESLRLMEASFGDTGLWKINTVTRCHESACGRVTSVLSFPAFTAK 300
CC 307 YGYKNCRLIYNGDGTGRGTHLSLFFVVMKGPNDALLRWPNQKVTMLLDQNNREHVID 366
CC 301 YGYKLCLELYNGDGTGRGTHLSLFFVIMRGEYDALLPWPFRNKVTFMLLDQNNREHAID 360
CC 367 AFRPDVTSSQRPVNDNNIASGCLFCVPSKMEA-KNSVYRDDAIFKAIQVD 418
CC 361 AFRPLSSASFQRPQSETNVASGCLFFPLSKLQSPKHAYVYKDDTNFLKQIVE 413
CC -----
RESULT 13
TRA3 MOUSE
ID TRA3 MOUSE STANDARD; PRT; 567 AA.
AC Q60803; Q62380;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)
DE (CRAF1) (TRAFAMN).
GN Name=Traf3; Synonyms=CRAF1, Trafam;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND INTERACTION WITH TNFRSF5.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=96299439; PubMed=8660894;
RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,
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RA Dinulos M.B., Distche C.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Lacy E.;
RT "A candidate gene for the amionless gastrulation stage mouse mutation
RT encodes a TRAF-related protein.";
RL Dev. Biol. 177:274-290(1996).
CC -!- FUNCTION: Adapter protein and signal transducer that links members
CC of the tumor necrosis factor receptor family to different
CC signaling pathways by association with the receptor cytoplasmic
CC domain and kinases. Seems to be involved in activation of NF-
CC kappa-B and JNK and in apoptosis. Is regulated by TANK/ITRAF which
CC competes with TNFRSF5/CD40 for binding. Seems to play a role T-
CC cell dependent immune responses (By similarity).
CC -!- SUBUNIT: Homotrimer (probable). Heteromer with TNFRSF3,
CC TNFRSF4, TNFRSF8/CD30, TNFRSF17/BCMA and EDAR, MAP3K5, MAP3K14,
CC and TRAF-interacting protein TRIP and TRAF and TNF receptor
CC associated protein TRAF. Binds to TANK/ITRAF (By similarity).
CC -!- TISSUE SPECIFICITY: In adult, highest in brain. Also found in
CC kidney, heart, thymus, spleen, lung, muscle, testis and ovary. Not
CC found in liver.
CC -!- DEVELOPMENTAL STAGE: In the embryo, expressed from E6.5 with
CC highest levels found between E11.5 and E13.5. At late stages of
CC gestation, from E14.5, only low levels are detected.
CC -!- DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
CC domains.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC -!- SIMILARITY: Contains 2 TRAF-type zinc fingers.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; U21050; AAC52175.1; -
EMBL; U33840; AAC52710.1; -
PIR; I49272; I49272.
HSP; Q13114; 1FLX.
MGD; MGI:108041; Traf3.
InterPro; IPR002083; MATH.
InterPro; IPR008974; Traf like.
InterPro; IPR001841; Znf_Ring.
InterPro; IPR001293; Znf_TRAF.
Pfam; PF00917; MATH; 1.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF02176; zf-TRAF; 2.
SMART; SM0061; MATH; 1.
SMART; SM00184; RING; 1.
PROSITE; PS50144; MATH; 1.
PROSITE; PS00518; ZF_RING_1; 1.
PROSITE; PS50089; ZF_RING_2; 1.
PROSITE; PS50145; ZF_TRAF; 2.
KW Apoptosis; Coiled coil; Repeat; Zinc-finger.
FT ZN_FING 67 76 RING-type.
FT ZN_FING 134 189 TRAF-type 1.
FT ZN_FING 190 248 TRAF-type 2.
FT DOMAIN 266 337 Coiled coil (Potential).
FT DOMAIN 414 559 MATH.
FT CONFLICT 72 73 CE -> WQ (in Ref. 2).
FT CONFLICT 390 390 T -> M (in Ref. 2).
SQ SEQUENCE 567 AA; 64263 MW; 2522B343B41192DC CRC64;
Query Match 33.0%; Score 730; DB 1; Length 567;
Best Local Similarity 32.1%; Pred. No. 4.7e-43;
Matches 187; Conservative 80; Mismatches 131; Indels 184; Gaps 22;
CC 1 MAASVTPFGSLELLQP-----GFSKTLGLTKLEAKYLCACNRVLRPFQA 47
CC 7 MDAAGTLQPNPLKLPDRGAGSVLPVPGGYKEKFKVT-VEKYKCKEKLVLNCPKQT 65
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QY 48 QCGHRYCSPCLASILSSGPQNCACVHGEIYBEGISILESSAPPPNAAARVESLPAVC 107
Db 66 ECGRFCESCMAALLSSSPKCTAC-QESIIRKQV-----FKDNCCKREILAQVYC 116
QY 108 PSD--GCTWKGTL-----KEYEFO-----DHYK-----TC 130
Db 117 RNEGRGCAEOLTLGHLVHLKNCQFEELPCLPADCKEKVLKDLRDHVEKACKYREATC 176
QY 131 GKCR--VP-----CRFHAI 142
Db 177 SHCKSQVPMIKLOKHEDTDCPCVVVSCPHKCSVQTLRLSELGAHLSECVPNAPSTCSFKRY 236
QY 143 GCLETVEGEKQO--EHEVQWLRHLAML--LSSVLEAKPLIGDQSHAGSELLQRCESLXK 198
Db 237 GCY--FQGTNQQTAKAHSASAVOHVLLKWSNLEKK-----VSLQON-ESVBK 283
QY 199 KTA--TFENIVCVLNREVER-----VAMTAEAGS-----RQHR 229
Db 284 NKSIQSLHNGICFSEIEIERQKEMLRNNSKILHLQRVIDSQAELKELDKELRIPRQNW 343
QY 230 LDDP----KTEALSSKVOOLE-----RSIGLKDLAVADLEQ 261
Db 344 EADSXKSSVESIQNRVTELESVDKSGAQAARNTGLLESQSLRHDTLSVHDIRLADMDL 403
QY 262 KVLEMEASTVDGVFIWKISDPARKLOEAVAGRIPAFYTSRYGYKMCRLIYINGDG 321
Db 404 RFQVLETAGVINGVLIKIRDYKXKQEVNGKTLISYQPFYTYGYGYKMCARVYINGDG 463
QY 322 TGRGTHLSLFFVVKNGPNDALLRWPKNQKVTMLLDQ--NNREHVIDAFPPDVTSSSQRP 380
Db 464 MGRGTHLSLFFVFMRGYDALLFPWPKQVKVTMLMDQSSRRHLGDAFPDPNSSFPPK 523
QY 381 VNDMNIASGCPPLPCPYSKMEAKNSVYRDDAIFIKAIVDLTGL 422
Db 524 TGEWNIASGCPVPVAVTVLE-NGTYIKDITFIKIVDITSL 564

RESULT 14
Q8CE28
ID Q8CE28 PRELIMINARY; PRT; 409 AA.
AC Q8CE28;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:473249E14 product:tnf receptor-associated factor 1,
DE full insert sequence.
GN Name-Trafi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX the FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
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RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076661;
RA Shibata K., Itoh M., Azawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Azawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK029135; BAC26315.1; --
DR HSSP; Q12933; 1CZY.
DR MGD; MGI:101836; Trafi.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
DR Receptor.
KW SEQUENCE 409 AA; 45464 MW; ADD7F997169D9AAD CRC64;
SQ
Query Match 33.0%; Score 729; DB 2; Length 409;
Best Local Similarity 38.7%; Pred. No. 3.7e-43;
Matches 158; Conservative 62; Mismatches 112; Indels 76; Gaps 6;
QY 85 LESSAPPDNNARVESLPAVCSDG----CTWKGTLKEYEPDQHVKTCKCR----- 134
Db 1 MASSAPPDENEFQFCPPAPCQDSEPRVLCT--ACLSENLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRFHAIGCLTVEGKQCEHVQLREHLAMLSSVLE 174
Db 59 VPGSPLTQEKVHSDVAEAEIMCFAGVCGSKGSPQSMQHEATSOSSHLVLLAVLKE 118
QY 175 AKPLLGPQSHAGSELLOR-----CES----- 195
Db 119 WKSPFGNGLSGAPMALERNLSELQQAAEATGDLVDVCRAPCCESQELALQHLVKEK 178
QY 196 ----LEKKTATFENIVCVLNREVERVAMTAEACSRHRLDQDKTEALS SVQLERISGL 251
Db 179 LLAQLEEKLRVFANIVAVLNKEVEASHLAASAASHQSLDREHILSLQEVVEQLQTLAQ 238
QY 232 KDLAMADLEQKVLMEAEASTVDGVFIWKISDPARKLOEAVAGRIPAFYTSRYGYK 311
Db 60,770 full-length cDNAs.";
```

Db 239 KDVLGKLEHSLRLMEASFDTGLFKITNTVKRCHESVCGRVSLSPAFYAKYGYKL 298
QY 312 CLRIYNGDGTGRGHLSLFFVWVGPNDAALLRPENQKVTMLDDQNNREHVIDAERPD 371
Db 299 CLRLYNGDGGGKTHLSLFIIVMRGEYDALLPFRNKVTFMLDDQNNREHAIDAFRPP 358
QY 372 VTSSSFQRPVNDMNIAASCPFCPVSKMEA-KNSYVRDDAIFIKAIYD 418
Db 359 LSSASFQRPQSETNVASSCPFLFFPLSKLQSPKHAYVKDDTWFCLKCIVD 406

RESULT 15
TRAF1_MOUSE
ID TRAF1_MOUSE STANDARD; PRT; 409 AA.
AC P39428;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TNF receptor associated factor 1.
GN Name=Trafi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 123-135 AND 390-402, AND INTERACTIONS
RP WITH TRAF2 AND TNFRSF1B.
RX MEDLINE=94349371; PubMed=8069916;
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
RN [2]
RP INTERACTION WITH TRAF1.
RX MEDLINE=97258620; PubMed=9104814;
RA Lee S.-Y., Choi Y.;
RT "TRAF1-interacting protein (TRIP): a novel component of the tumor
RT necrosis factor receptor (TNFR1)- and CD30-TRAF signaling complexes
RT that inhibits TRAF2-mediated NF-kappaB activation.";
RL J. Exp. Med. 185:1275-1285(1997).
CC -!- FUNCTION: Adapter protein and signal transducer that links members
CC of the tumor necrosis factor receptor family to different
CC signaling pathways by association with the receptor cytoplasmic
CC domain and kinases. Mediates activation of NF-kappa-B and JNK and
CC is involved in apoptosis. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.
CC -!- SUBUNIT: Homotrimer (Probable). Heteromer with TRAF2 and
CC associates with TNFRSF1B/TNFR2 through TRAF2. Associates with
CC TNFRSF1A/RANK, TNFRSF18/AITR, TNFRSF17/BCMA, TNFRSF19/TROY,
CC TNFRSF19L/RELT, XEDAR, EDAR, TANK/ITRAF and RIPK2 (By similarity).
CC Interacts with BIRC2 and BIRC3 N-terminus (By similarity). Binds
CC TRAF1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- DOMAIN: The coiled coil domain mediates homo- and hetero-
CC oligomerization.
CC -!- DOMAIN: The MATH/TRAF domain binds to receptor cytoplasmic
CC domains.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L35302; AAC37663.1; -.
CC PIR: A54750; A54750.
CC HSSP: Q12933; 1CZY.
CC MGD: MGI:101836; Trafi1.
CC InterPro: IPR002083; MATH.

DR InterPro: IPR008974; Traf_like.
DR Pfam: PF00917; MATH; 1.
DR SMART: SM00061; MATH; 1.
DR PROSITE: PS0144; MATH; 1.
KW Apoptosis; Coiled coil; Direct protein sequencing.
FT DOMAIN 167 256 Coiled coil (Potential).
FT DOMAIN 259 405 MATH.
SQ SEQUENCE 409 AA; 45464 MW; EBA7FBE5639FEDDF CRC64;
Query Match 32.9%; Score 727; DB 1; Length 409;
Best Local Similarity 38.5%; Pred. No. 5.1e-43;
Matches 157; Conservative 63; Mismatches 112; Indels 76; Gaps 6;
QY 85 LESSAFPPDNAARREVELPAPVCPDGDG---CTWKGTLKEYEFQDHVTKCKCR----- 134
Db 1 MASSAPDENEFQCGPPAPCDPSEPRVLCCT--ACLSENLRDDEDRICPKCRADNLHP 58
QY 135 -----VPCRPHAIGCLTVEGEKQOEHEVQWLEHMLAMLLSSVLE 174
Db 59 VSPGSLTQEKVHSDVAEAEIMCPFAGVCGSPQSMQHEATSQSHLYLLLAULKE 118
QY 175 AKPLLLGDQSHAGSELLQR-----CES----- 195
Db 119 WKSSFGSNGSAPMALEENLSLQQAQAEATGDLVDVCRAPCCESOEELALQHLVKEK 178
QY 196 ----LEKKTATATTENIVCVLNREVERVAMTAACSRQHLDDQDKIEALSCKVQOLERSIGL 251
Db 179 LLAQLEEKLRVPANTVAVLNKEVEASHLAAASHQSQLDREHLLSLEQRVVLELQTLAQ 238
QY 252 KDLAMADLEQKYLEMEASTYDGVFTWKISDFARKLQEAAGRIPAIFSPAFVTSRYGYKM 311
Db 239 KDQVLGKLEHSLRLMEASFDTGLFKITNTVKRCHESVCGRVSLSPAFYAKYGYKL 298
QY 312 CLRIYNGDGTGRGHLSLFFVWVGPNDAALLRPENQKVTMLDDQNNREHVIDAERPD 371
Db 299 CLRLYNGDGGGKTHLSLFIIVMRGEYDALLPFRNKVTFMLDDQNNREHAIDAFRPP 358
QY 372 VTSSSFQRPVNDMNIAASCPFCPVSKMEA-KNSYVRDDAIFIKAIYD 418
Db 359 LSSASFQRPQSETNVASSCPFLFFPLSKLQSPKHAYVKDDTWFCLKCIVD 406

Search completed: November 10, 2004, 16:28:16
Job time : 200 secs